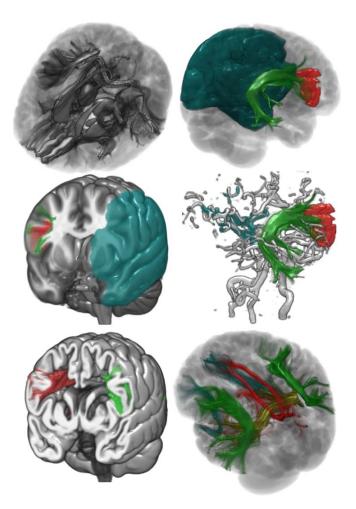
# Connectopedia

## Version 2.6



# Interactive Atlas of Humain Brain Functions, Connectomics and Vasculature

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Acknowledgment : Pr Chris Rorden, McCausland Center, University of South Carolina, USA

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#### I. General Overview

Connectopedia is an interactive atlas of human brain structures, functions and vasculature, using brain connectomics to assess functional pathways of the tasks performed by the brain.

Connectopedia is linked with the DPTOOLS package from version 6 and above, and is distributed standalone, free of charge, for academic purposes only, with BSD licensing.

Connectopedia was coded using C++ and Delphi, with OpenGL 2D and 3D reconstructions for volume rendering purposes (thanks to the Chris Rorden MRIcroGL sources), and is compatible with NIFTI files. Connectopedia requieres Microsoft Windows Vista or Mac OSX 10.8 and above, a minimum of 4 GB of RAM (8 recommended), and an OpenGl capable graphic card. A display capable of 1080p or two displays are recommended.

Connectopedia uses the 152 MNI T1 and Cortical Areas (116 areas) Atlas templates for 3D rendering of the structural grey matter of the brain. The 58 Fiber bundles were reconstructed from my own brain, using HARDI 60 directions, b value of 1500, and automatically generated and coregistered to the T1 MNI template using DPTOOLS 6.1 and the MedInria 1.9 software suite. The 90 arterial and 54 venous referenced structures were set by manual segmentation on the T1 MNI 152 isotropic 1 mm<sup>3</sup> template. Arterial and Venous 3D VR reconstructions were set on TOF and 3D Phase Contrast MR sequences and isotropically 1 mm<sup>3</sup> coregistered to the T1 MNI template.

Connectopedia was created to provide to neuroscientists as well as students an easy way of learning, teaching or checking functional neuroanatomy, and is linked to DPTools v6 and above, which was used to study structural and functional connectomics with real time reconstructions and assessment of the brain structural and functional connectoms using RTConTrack.

RTConTrack, acronym for Real Time Connectom Tracking, is a special algorithm dedicated to identifying the Brain Grey and White Matter Structures involved in the Brain Functions occurring during a fMRI performed task, and to creating dynamic maps of their information exchanges patterns.

RTConTrack can be compared to a « GPS » system, where the « Cities » are the Grey Matter Structures, the « Highways » the White Matter Bundles, and the « Cars » the neuronal informations going through specific maps, each map characterizing a specific brain function.

To be able to identify those structures and informations, RTConTrack uses functional fMRI Bold activation maps, analyzed in « Pseudo Real-Time » using a dedicated interpolation algorithm (Static fMRI maps are not accurate enough for this purpose) in order to see the informations going from one « city » to another, and Diffusion MRI sequences to individualize the «Highways» using Tractography (HARDI sequences).

To identify the Grey and White Matter Structures involved in a specific function, RTConTrack uses dedicated Brain Functional and Structural Anatomy Atlases.

When those structures are identified, RTConTrack computes the Structural and Functional Dynamic Connectoms maps involved in all functions performed by the Brain during the fMRI acquisition.

When the Structural and Functional Connectoms are computed for each fMRI activation Timeline, RTConTrack reconstructs in 4D the Connectoms evolutions patterns.

Then RTConTrack back reconstructs the identified Grey and White Matter structures to match the Anatomy Templates in a Dynamic Anatomy Activation Mapping and in a Dynamic 4D (Time and Space) Functional Anatomic Reconstruction.

These Dynamic Functional Anatomic and Connectomic Reconstructions are then coded into «GPS» maps, and these maps and compared using an artificial intelligence algorithm with other similar maps included in a dedicated database, to assess similarity scores among the known brain functions, the tasks and the subjects.

Brain Functions occurring during the fMRI acquisition are then identified, compared and scored, and a report is generated with percentage of Occurrences for the Major and Minor identified brain functions.

These scores can then be used to assess the therapy efficacy (brain functions occurrences variations before and after treatment) in psychiatric patients (depressed, schizoid, autistic ...), in coma patients (existence of emotional and cognitive processes during e.g. an auditory stimulation), in lie detection, in consumer satisfaction scores, aso...

From the 2.2 version and above of Connectopedia, multithread processing is enabled (speeds up to 250% the rendering and analysis functions), and 408 identified brain functions (from behavior to cognitive or emotional patterns, aso...) are included and referenced in the Connectopedia Explorer database and within the RTConTrack algorithm, as well as on the web site.

Version 2.3 enables the vascular and structural anatomy labeling, as well as importing and coregistering Raw Gis map files from DPTools (diffusion/perfusion/activation maps) using the 'Drag and Drop' feature of the 3D Renderer window (MS Windows version only).

Version 2.4 has improved Connectoms rendering of the Grey and White Matter Structures connections with simplified views of the connected items and skeleton view of the global structures connections, as well as interactive selecting process of the connectomic mapping of Grey and White Matters.

Version 2.5 has a simplified 'Sequencer Window' interface and new filtering features to explore the Brain Functions.

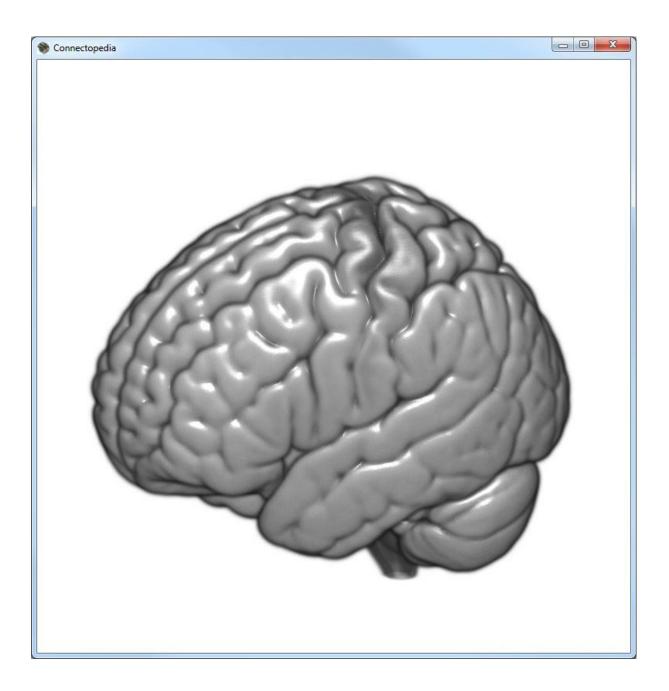
Version 2.6 has Statistics Functions for Single Subject or Group Analysis and assessment of the Effective Connectomics and Brain Functions Usage comparison through Time.

Neuro-functional and vascular knowledge database were set using Wikipedia, and some other references:

- 1. Bases of Functional Neuroanatomy, Monica Baciu, de Boeck Editions, 2011
- Fiber Pathways of the Brain, Jeremy Schmahmann, Deepak Pandya, Oxford Editions, 2006
- 3. Networks of the Brain, Olaf Sporns, MIT Press, 2011
- Atlas of Human Brain Connections, Marco Catani, Michel Thiebaut de Schotten, Oxford Editions, 2012
- 5. Diagnostic Imaging Brain, Ann Osborn, Elsevier 2005
- 6. Brain Vasculature, G. Lazorthes, Masson 1961.

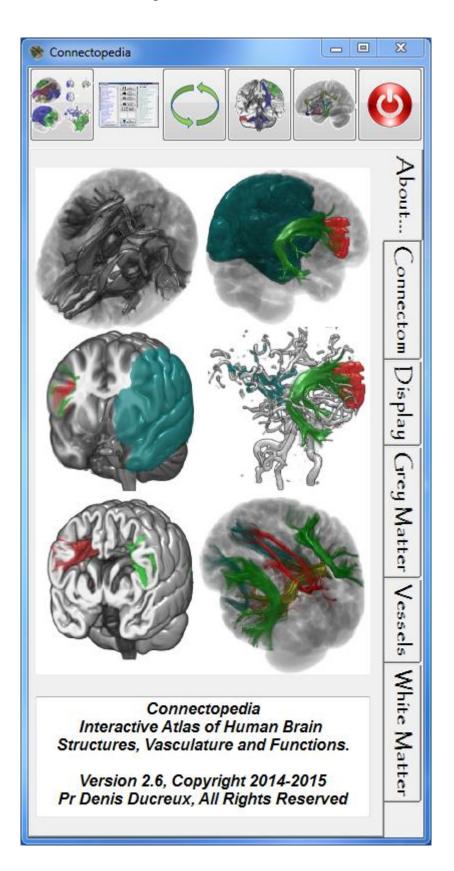
## Connectopedia includes :

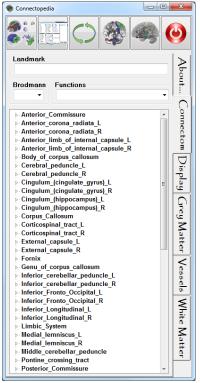
- The **3D Rendering** viewer window of brain cortex (only grey matter), brain (grey and white matter), fiber bundles and vasculature (arteries and veins):



Analyze '.img/hdr' or NIFTI '.nii' files may be imported using the 'Drag and Drop' feature of this 3D Renderer window, as well as DPTools Raw Gis map files (with or without prior co-registering).

- The **Selector** window with specific buttons and tabs:





\* The Connectom Tab:

- a brodmann area (BA) selector, with all BA linked to cortical areas and to brain functions

- a brain function (BF) selector linked to the BA selector

- a connectom path selector to select either bundle by bundle, area by area, areas by bundles, or bundles by areas, showing how cortical areas are structurally linked to each other by the fiber bundles, as well as vasculature branches treeview

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Render All Items			

\*The Display Tab:

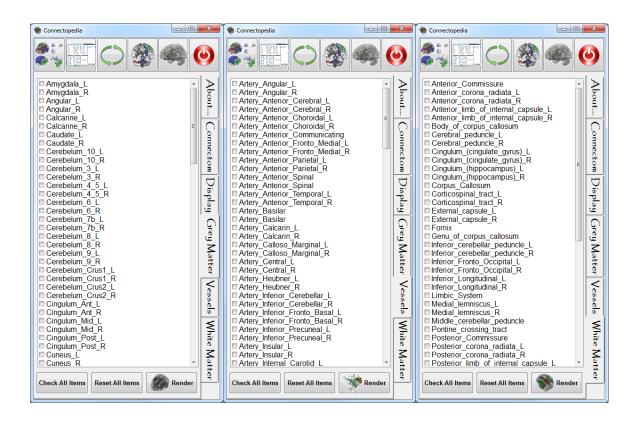
Display settings :

- Quality
- Alpha Blending
- Minimum and Maximum Thresholding
- Items color setting

Clipping and Cutout Tools

"Render All Items" button

#### \*The Grey Matter, Vessels, White Matter Tabs:



to study or show either cortical areas and/or fiber bundles and/or vessels one by one or by group, sorted by Name or Topology (RC to select sorting type).

Buttons to check, uncheck all items, and to render the selected items in the 3D Render Window.

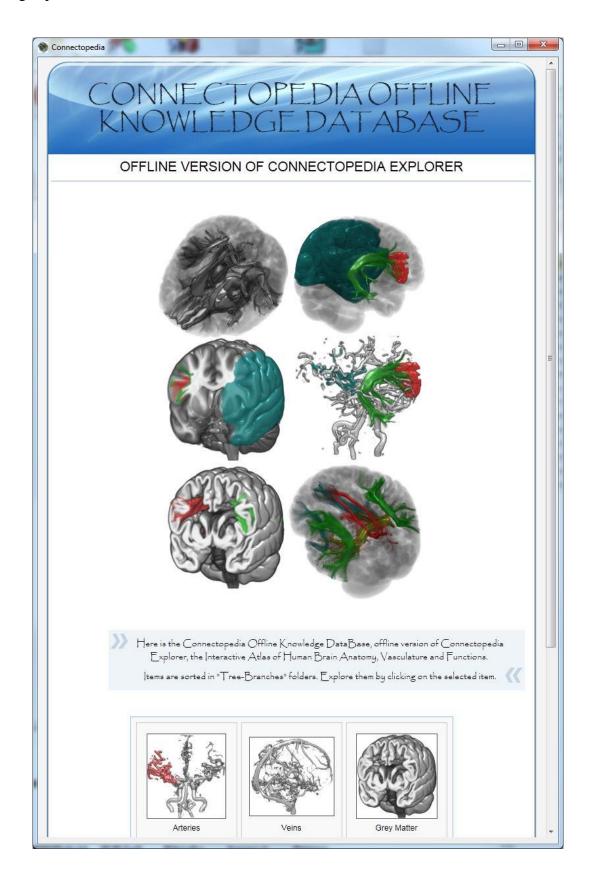
### \*Functions buttons:



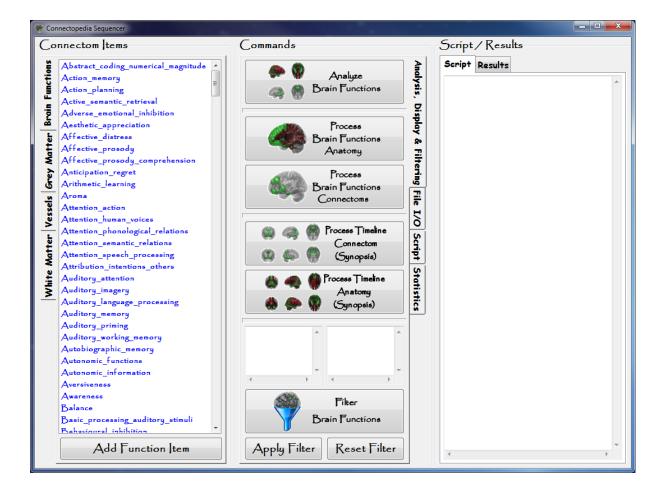
. the "KdB Enabler" Button to enable or disable Preview of the KdB Files, and selecting between Offline and Online KDB (RC on it to select DataBase source):

- the "Sequencer" Button to enable or disable the Connectopedia Sequencer Window
  the "Synchronize" Button to sync Connectopedia and DPTools
  The "Tracking Pathways" Button
  The "Movie" Button
- . the "Exit" Button

- The **Knowledge Database Browser** (KDB) with anatomical and functional descriptions of the grey matter areas, the white matter bundles, and the vasculature, either online if you have a high speed internet connection, or offline.



- The **Connectopedia Sequencer Window** to batch/script 2D/3D reconstructions, analyze the connectomic, analyze brain functions, ...

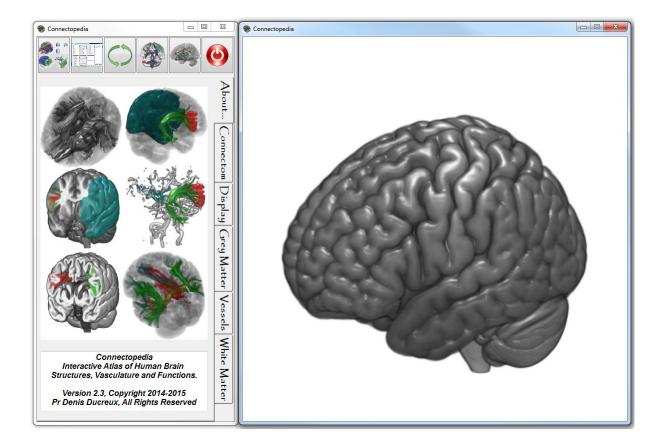


With Connectopedia user can select a fiberbundle, see the cortical areas linked by this bundle to each other, add vasculature to see the vascular territories, and view how the brain is working within this network using the Real Time fMRI Movie Selector.

User can also select two cortical areas and track the pathways linking the two.

When used combined to DPTools, user can automatically identify arterial or venous territory (stroke) and identify damaged brain structures.

All the movies of the brain included in the KdB are showing real time activations, and structural and functional connectomics involved in the selected functional task.



#### **II.** Installation

Standalone Connectopedia comes with two distributions, for Microsoft Windows Vista and above, and for Apple OSX 10.8 and above, each either online (lightweight client around 50 MB) or offline (<500 MB).

Requierements are: minimum of 4GB RAM (8 recommended), 500 Mo (for Windows and OSX Standalone distributions) or 2 GB of free hard disk space (for DPTools distribution), and an OpenGL compatible video card (embedded in chipset e.d. Intel, ATI, nVidia or separate card).

#### **II.I Windows installation:**

Download the software "Connectopedia-Install.exe" on the web site and double-click on it to install.

By default, installation directory (\$INSTDIR) will be DPTools related (e.g. C:\DPTools\bin\Connectopedia). One link will be created in the "Start Program" menu as "Connectopedia". To run the program, just click on this link.

#### **II.II OSX Installation:**

Download the software "XConnectopedia.zip" on the web site. When downloaded, double-click on it where it was downloaded (e.d. "Downloads" folder) to unarchive "XConnectopedia", then run the software by double-clicking on it.

Users of OSX 10.8 and Mavericks (10.9) should change the OSX Gatekeeper properties to be able to run XConnectopedia (see the "Troubleshootings" section of this manual).

## III. How to use it?

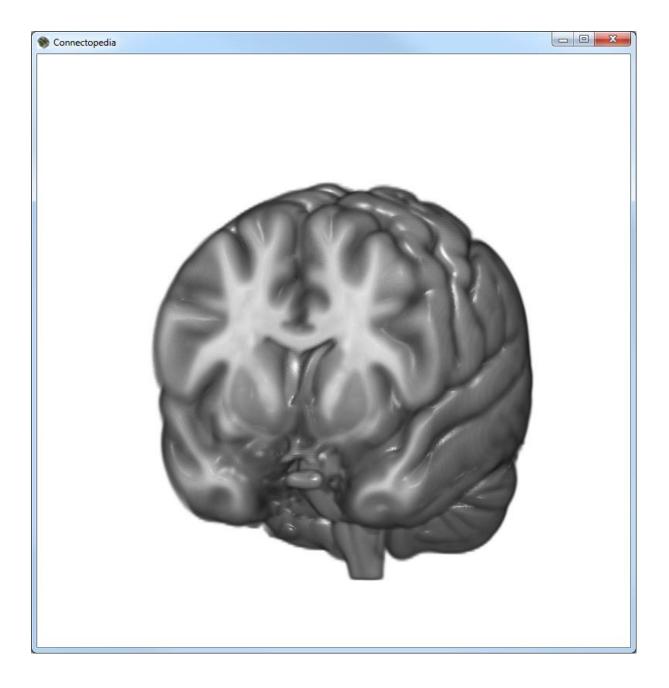
Menus are available using the Right button of the mouse (Right Click, RC) in the **3D Rendering Area**, the **Connectoms Path Selector**, the **Clipping Tool Panel** and the **Movie Selector**.



By RC on the **3D Render Window**, you can select either "Brain Views" with "Brain", "Brain Ghost", "Connectom", "Extracted Cortex" or "Virtual Dissection" sub-menus, "Vessels Views" with "Arteries" and "Veins" sub-menus reconstructions Templates, in 3D, 2D MPR Slices, or 2D mosaic slices.

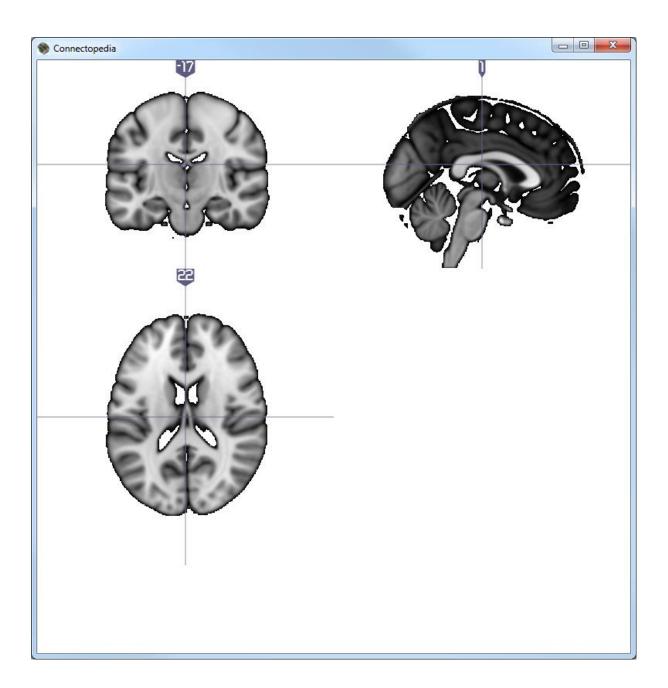
RC is also used to Zoom the 3D rendered view.

Using the Clipping bars below the Display area in Display Tab of the Selector Window, user can perform 2D or 3D clipping reconstructions of the selected Template.



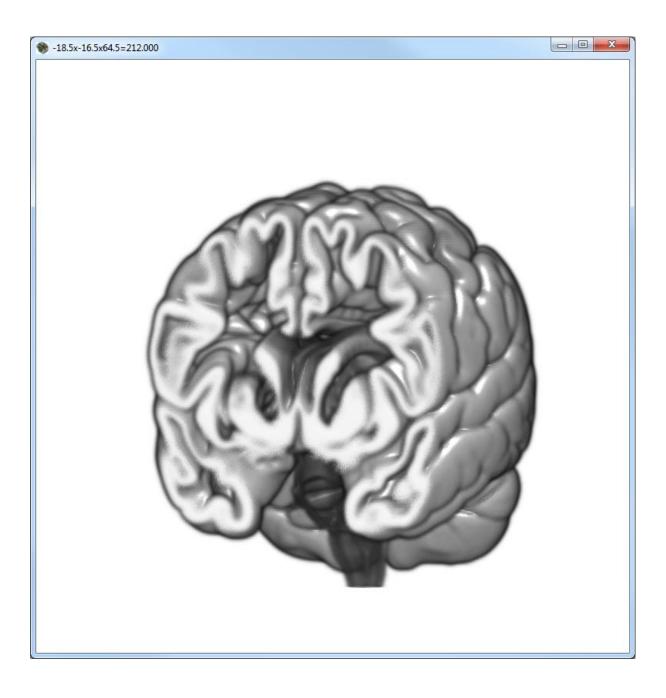
Here is a **3D Cut** using the "Brain" Template:

The matching **2D MPR** reconstruction:



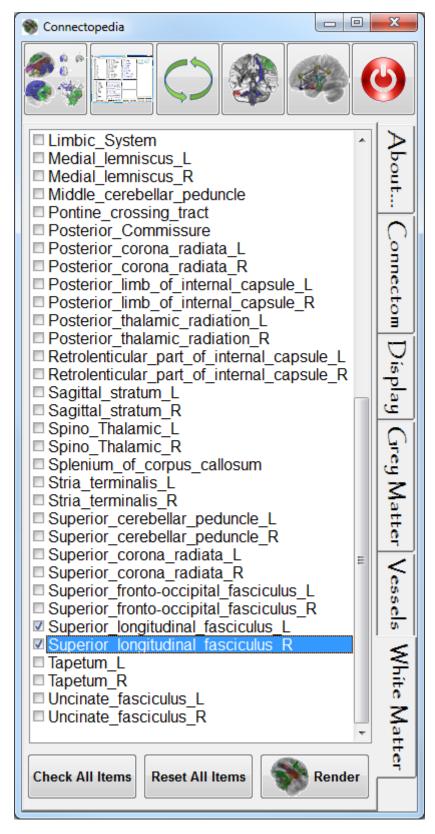
Note that given coordinates in 2D reconstructions are in true MNI coordinates.

Here is a **3D** Cut using the "Cortex" Template (in this template, only grey matter is reconstructed):



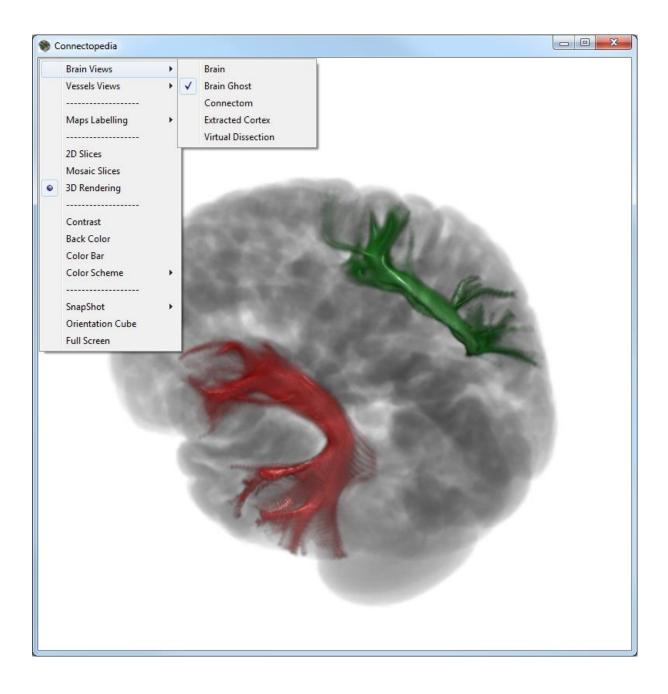
# IV. First exercise: Bundles selection

Let's study the both Superior Longitudinal Fasciculi, especially the Arcuate bundles.



First select in the White Matter Tab Selector the matching bundles (« Superior\_Longitudin al\_Fasciculus\_L and \_R ») by LC on the small empty square (to deselect it, just reclick), then set the "Brain Views" Template using RC on the 3D rendering area, then press the Render Button.

Choose the "Brain Ghost" submenu item by RC on the 3D Render window.



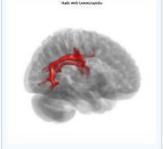
When selected, the KDB Window displays anatomo-functional informations related to the selected bundle or cortical area.

# CONNECTOPEDIA OFFLINE KNOWLEDGE DATABASE

#### SUPERIOR LONGITUDINAL FASCICULUS ← □ →

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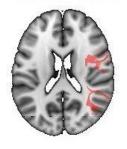
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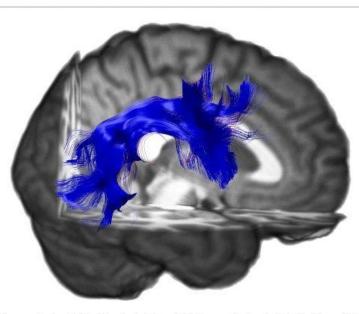


SUPERIOR LONGITUDINAL FASCICULUS

SUPERIOR LONGITUDINAL FASCICULUS AXIAL SLICES

Made with Connectopedia





The superior longitudinal fasciculus (also called the superior longitudinal fascicle or SLF) is a pair of long bi-directional bundles of neurons connecting the front and the back of the cerebrum. Each association fiber bundle is lateral to the centrum ovale of a cerebral hemisphere and connects the frontal, occipital, parietal, and temporal lobes. The neurons pass from the frontal lobe through the operculum to the posterior end of the lateral sulcus where numerous neurons radiate into the occipital lobe and other neurons turn downward and forward around the putamen and radiate to anterior portions of the temporal lobe.

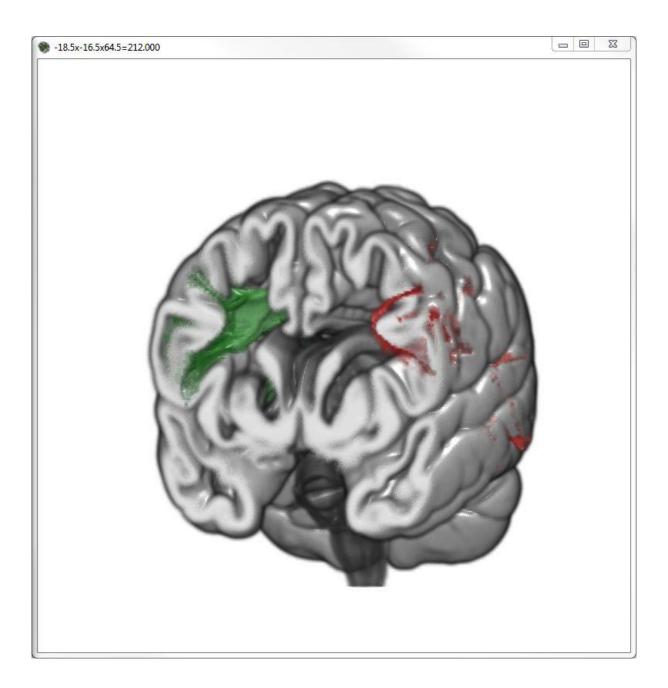
#### Anatomy

The SLF is composed of four distinct components SLF I, SLF II, SLF III, and arcuate fascicle (AF). In humans, these four components are bundled together although they are functionally separate. In non-human primates, the SLF and AF are anatomically separate and have separate trajectories.

#### SLF I

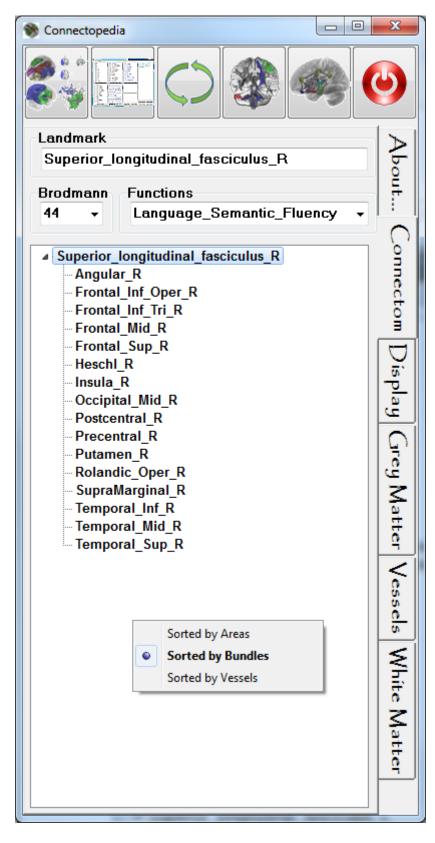
SLF I is the dorsal component and originates in the superior and medial parietal cortex, passes around the cingulate sulcus and in the superior parietal and frontal white matter, and terminates in the dorsal and medial cortex of the frontal lobe (Brodmann 6, 8, and 9) and in the supplementary motor cortex (M II).

The selected bundles can be viewed with the "Extracted Cortex" Template in 3D VR mode using a **3D Cut** clipping:



By LC in the Connectom Tab Selector on a cortical area (e.g. «Frontal\_Oper\_Inf\_L »), Brodmann areas referring to the selected cortical area are displayed in the BA selector.

You can select between all the displayed BA by Left Clicking on the **BA Selector**:



Informations in the **Connectom Tab** are restricted to the selected bundle.

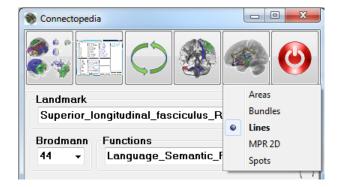
By LC on the triangle 4, a Connectoms Treeview displays all the cortical areas linked to each other by the selected bundle. You can sort these either by Areas, Bundles or Vessels by RC on the Connectom Path Selector and selecting the menu item.

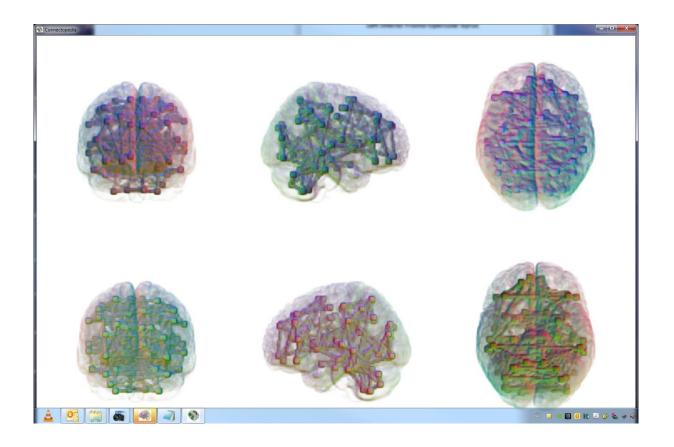
On the right side of the **BA Selector** is the **BF Selector**. When selecting a specific BA, functions are listed in the **BF Selector**, and can be selected by LC on it (here BA « 44 », and Function: « Language\_Semantic\_Flue ncy »). When the function is selected, movies showing the real time activation of the brain can be



displayed by LC on the Movie Viewer Button

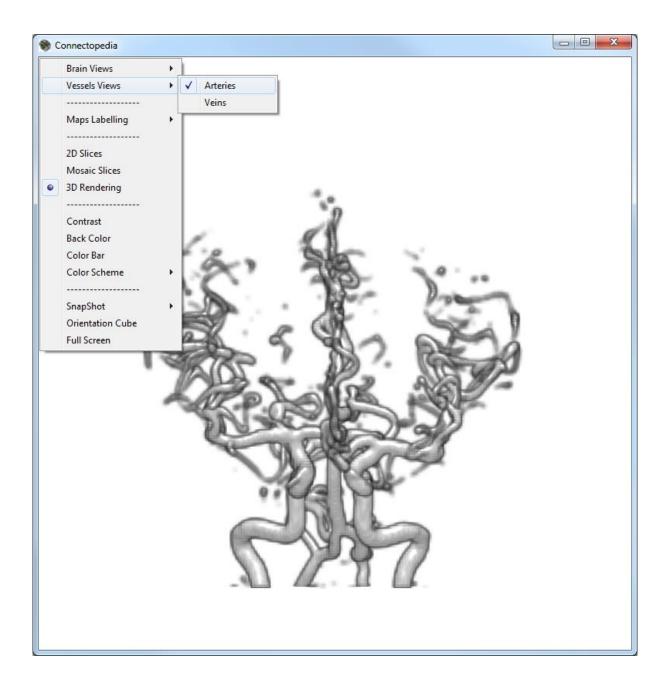
User can choose between "Areas", "Lines", "Bundles", "Spots", and "MPR 2D" movies, showing the brain connectivity in real time:



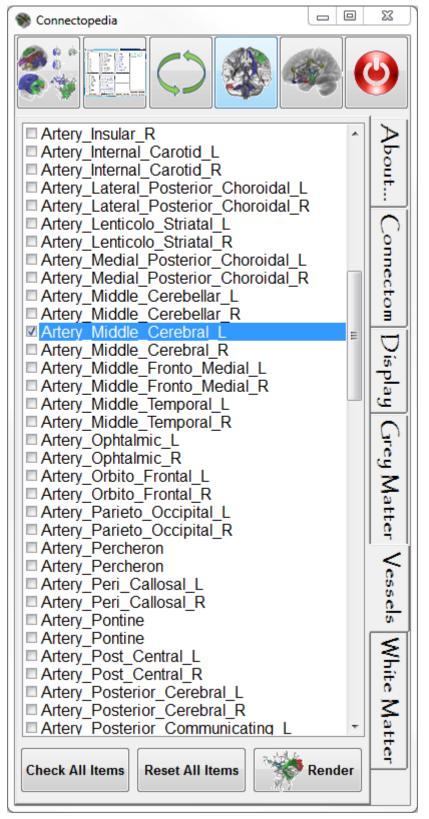


# V. Second exercise: Bundles and Arteries

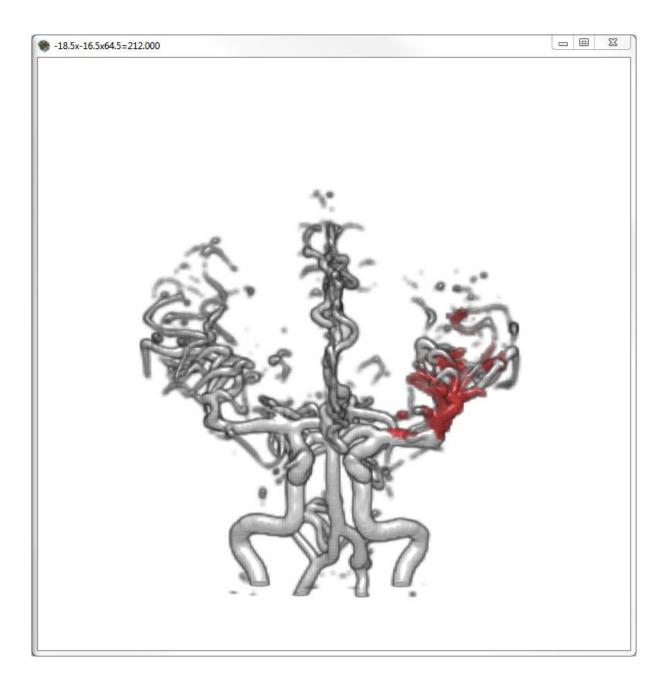
Connectopedia includes a vascular knowledge database of arterial and venous structures. User can reconstruct brain arteries using the "Arteries" Template in the "Vessels Views" menu of the 3D rendering window:



Let's now study the Left Middle Cerebral Artery combined with the Right Superior Longitudinal Fasciculus.



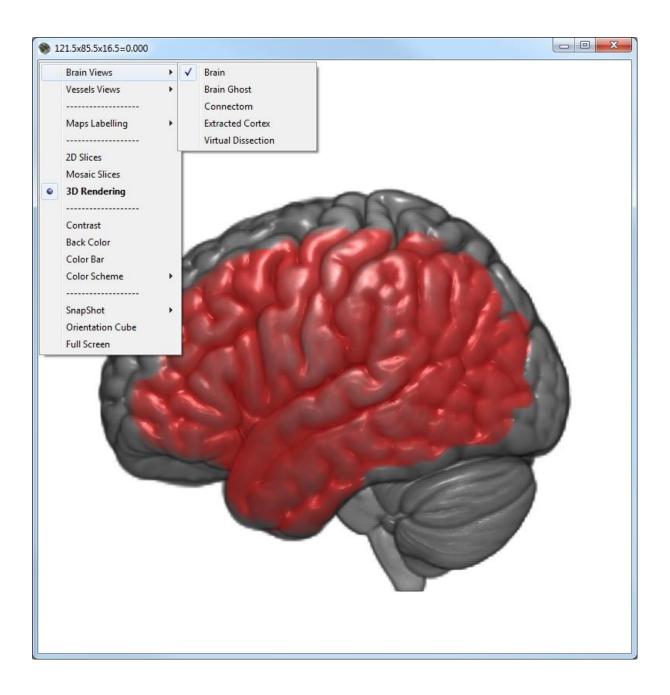
First select in the **Vessels Tab Selector** the matching artery (« Artery\_Middle\_Ce rebral\_L ») by LC on the small empty square (to deselect it, just LC again), then set the "Arteries" Template using RC on the 3D rendering area, then press the Render Button.



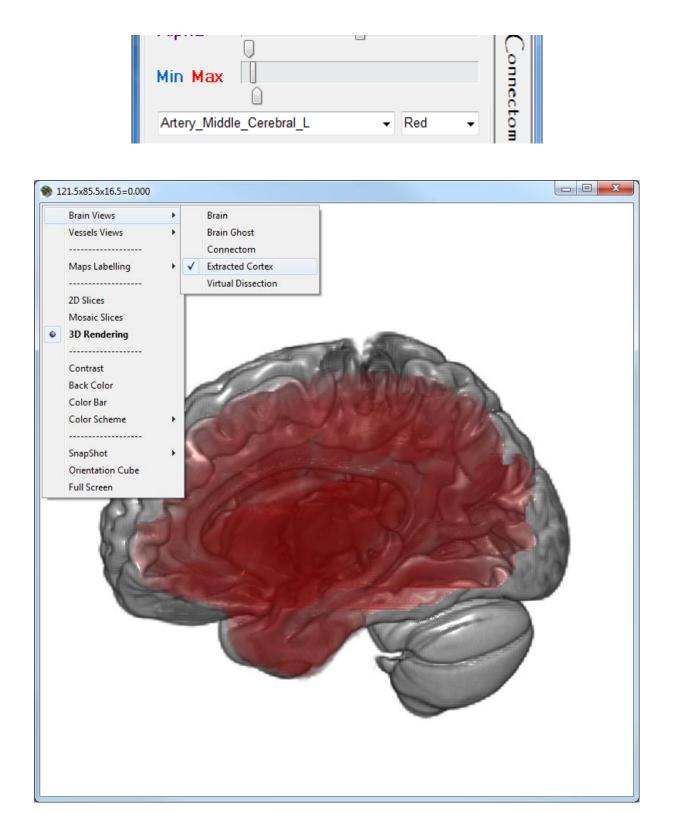
Let's now have a look at the 2D Slices of the Left MCA arterial territory. RC on the 3D Rendering area, select « 2D Slices » and also select the « Brain » Template in the "Brain Views" menu:



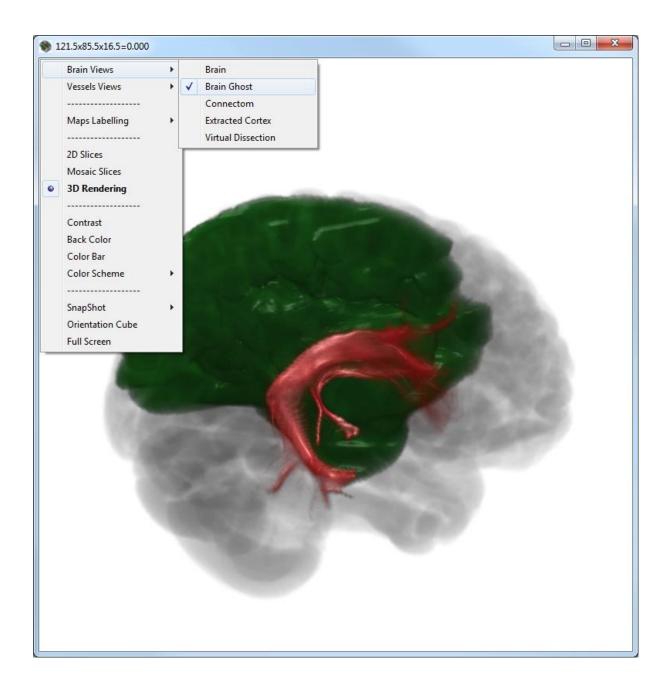
Now have a look at the 3D VR reconstruction of this arterial territory:



In the "Extracted Cortex" sub-menu item of the "Brain Views" Template, with "Display Settings" set to High Min and Low Max, some transparent view of the arterial territory:

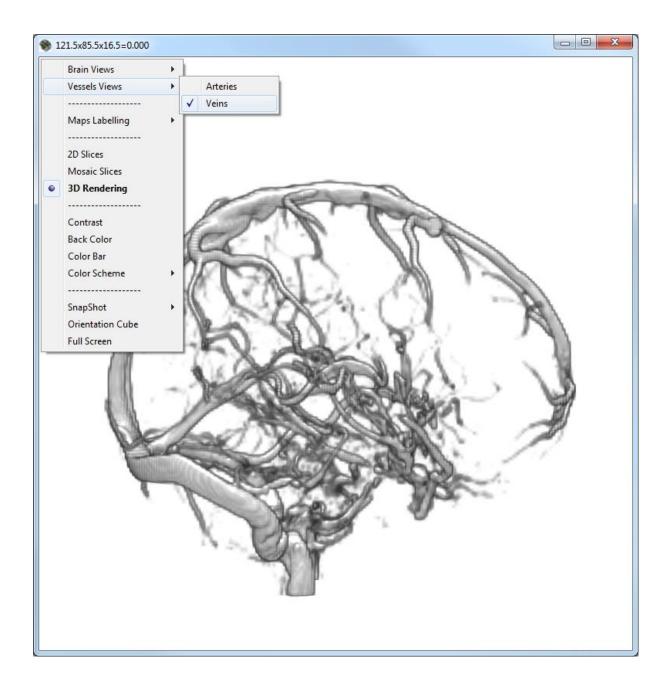


At last, combine this artery with the Right Superior Longitudinal Fasciculus by LC on the matching empty square in the **White Matter Tab Selector** and display these selected items using the "Brain Ghost" sub-menu of the "Brain Views" 3D VR Template (by RC on the 3D rendering area):

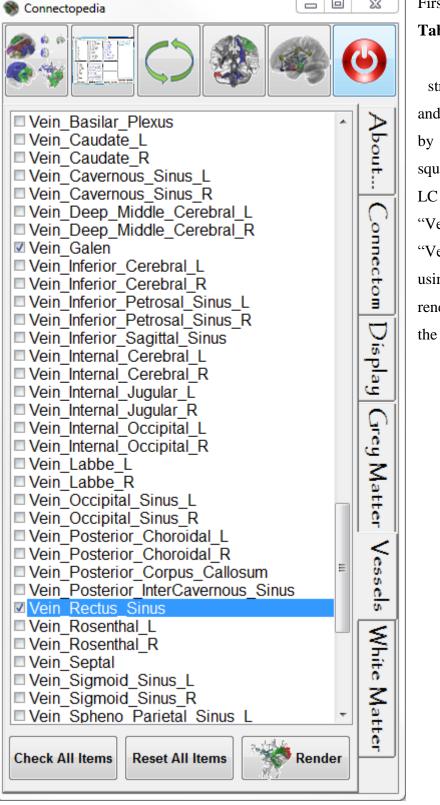


# VI. Third exercise: Grey Matter Structures and Veins

User can also reconstruct brain veins and venous sinuses using the "Veins" Template of the 3D rendering window:



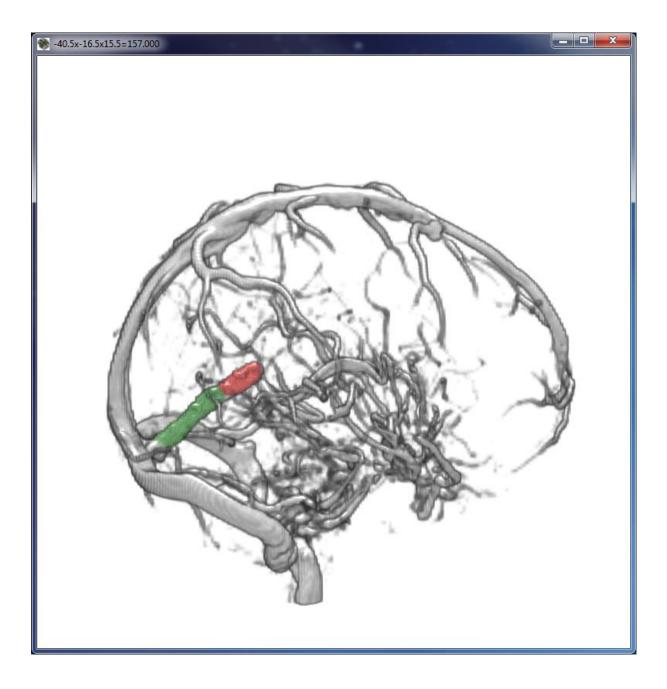
Let's now study the both Thalami combined with the Galen Vein and the Straight Sinus (e.g. in case of deep venous thrombosis).



First select in the Vessels Tab Selector the matching venous

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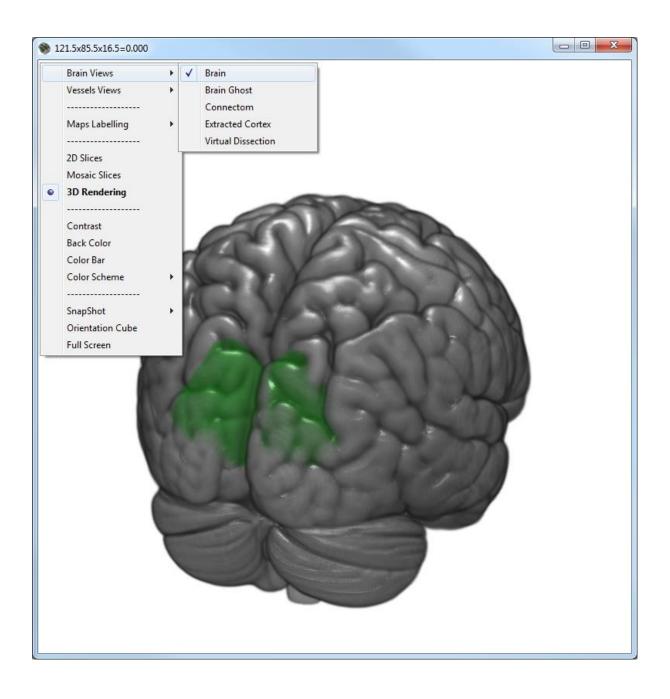
structures (« Vein Galen » and « Vein\_Rectus\_Sinus ») by LC on the small empty square (to deselect it, just LC again), then set the "Veins" Template in the "Vessels Views" menu using RC on the 3D rendering area, then press the Render Button.



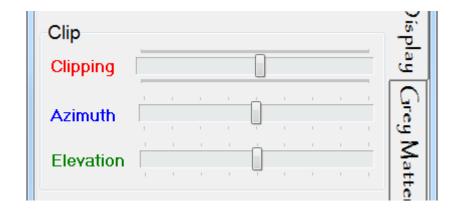


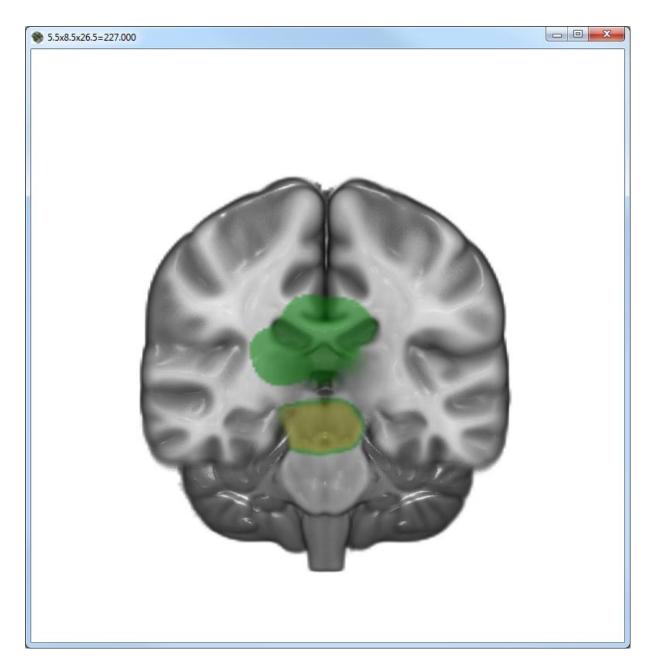
Now let's see how are these venous territories in 2D (RC on the 3D Rendering area, and select the « Brain » Template in the "Brain Views" menu , then the « 2D Slices »):

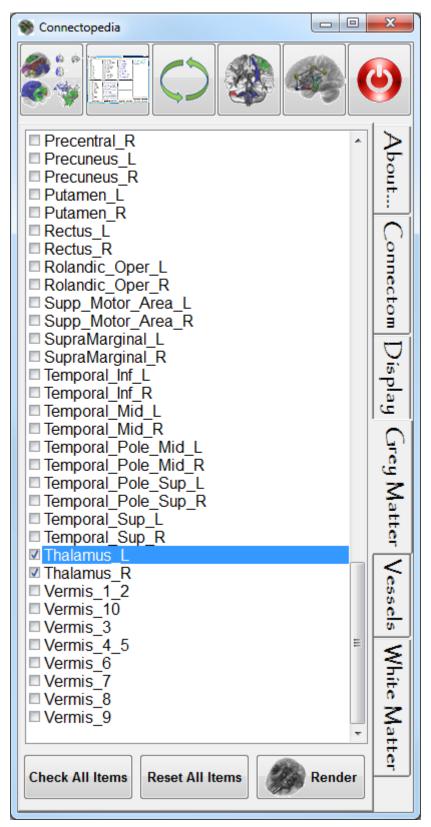
Let's see them in 3D (RC on the 3D Rendering area and select « 3D Rendering »):



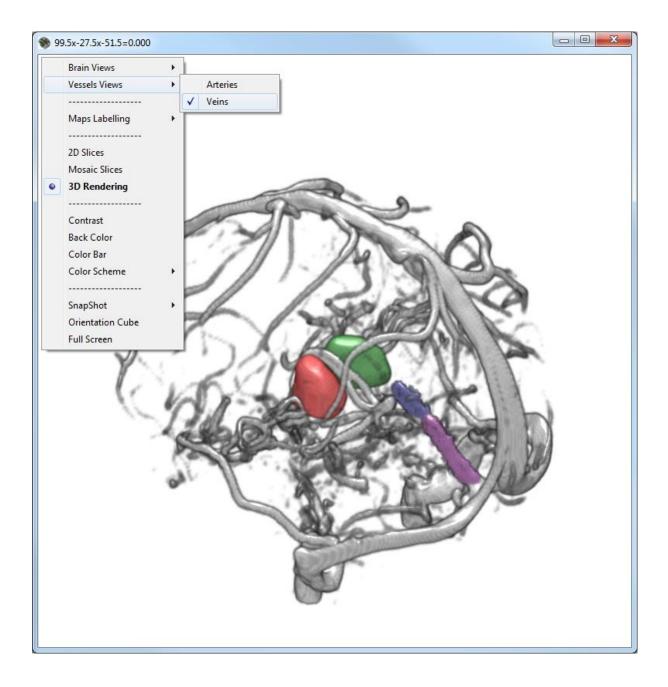
And inside the brain when applying the **3D Cut** Clipping Tool:



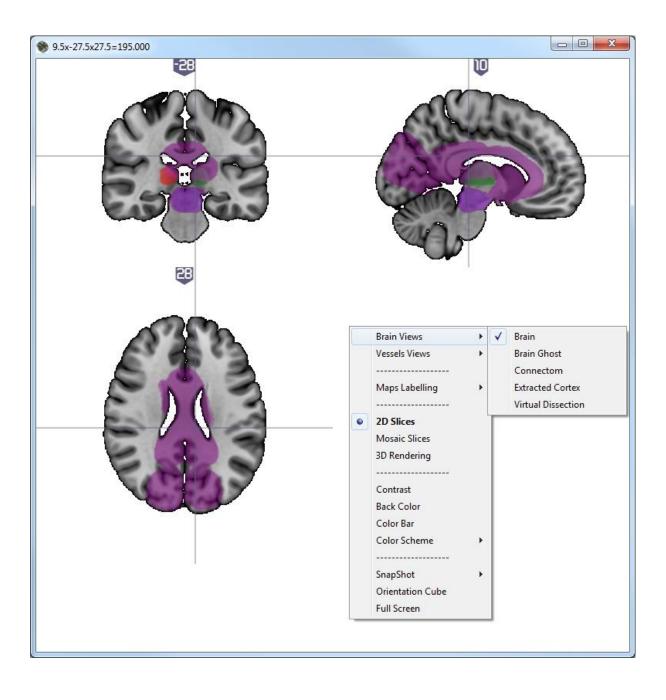




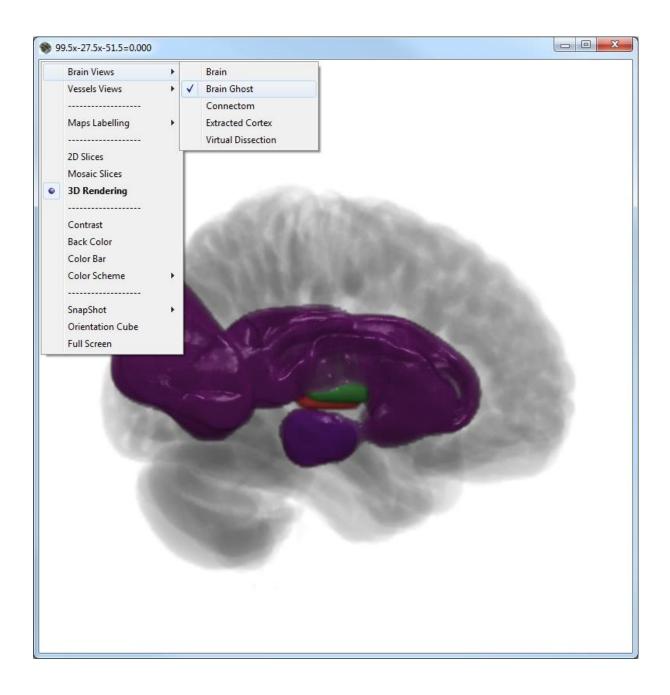
Now select the « Thalamus\_R » and « Thalamus\_L » by LC on the empty square in the Gery Matter Tab Selector, RC on the 3D and Rendering area to select the « Veins » Template of the "Vessels Views" menu again, showing venous and grey matter structures, then press the Render Button:



Let's see how these structures are each other intermingled in « 2D Slices » by RC on the 3D Rendering area and selecting the "Brain" Template of the "Brain Views" menu:



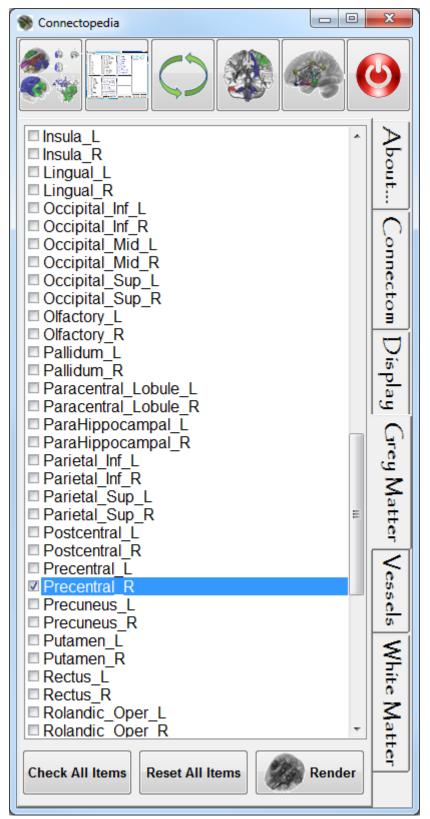
Now have a look at the 3D VR reconstruction of these structures by RC on the 3D Rendering area and selecting the "Brain Ghost" sub-menu of the "Bundles" Template:



Venous drainages are overlapping the both Thalami, as you can see.

# VII. Fourth exercise: Tracking fiber pathways between two cortical areas

Connectopedia includes an algorithm involved in automated identification of linked grey matter structures by white matter fiber bundles.

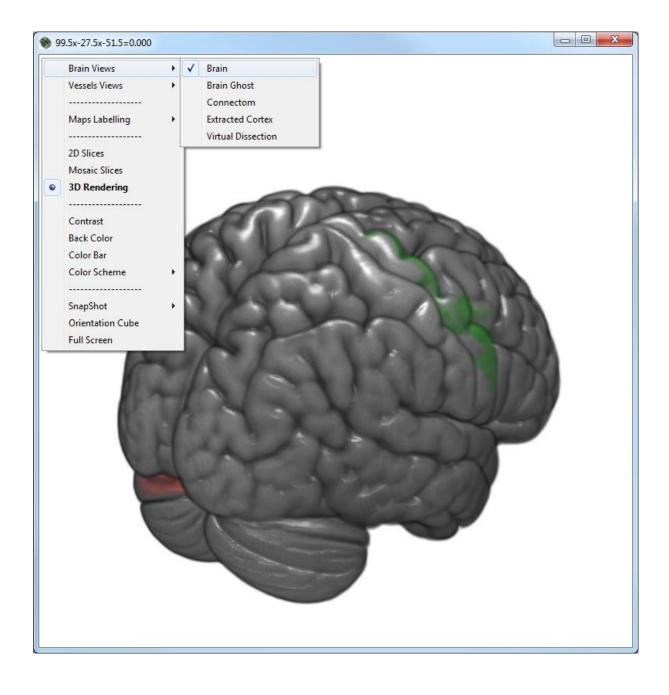


User can check the relations existing between grey matter areas using the "Tracking



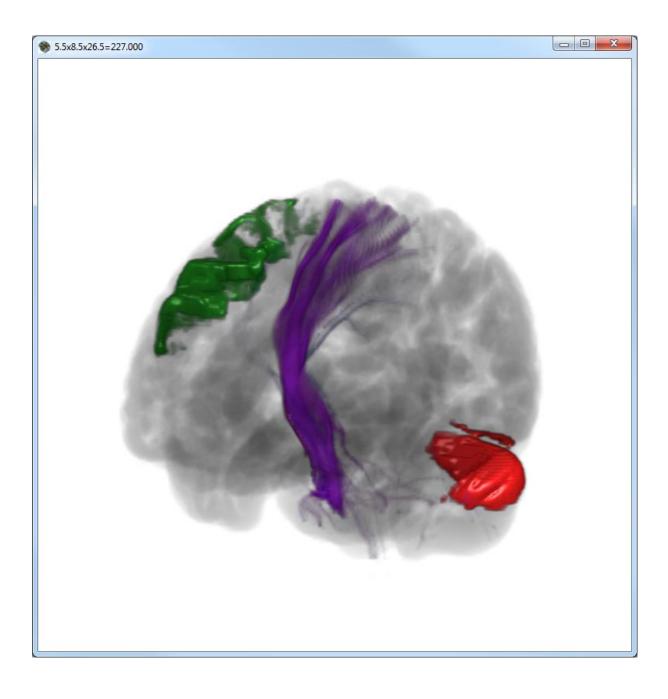
Pathways" Button

which Let's see fibers bundle(s) is (are) linking the "Right Pre-Central" cortical "Left area and the Cerebellum Crus 1". First select the cortical areas by LC on the empty square in the Grey Matter Tab Selector, then select the "Brain" Template of the "Brain Views" menu.



Then LC on the "Track Pathways" Button :	- A
Then LC on the "Track Pathways" Button :	<u> </u>

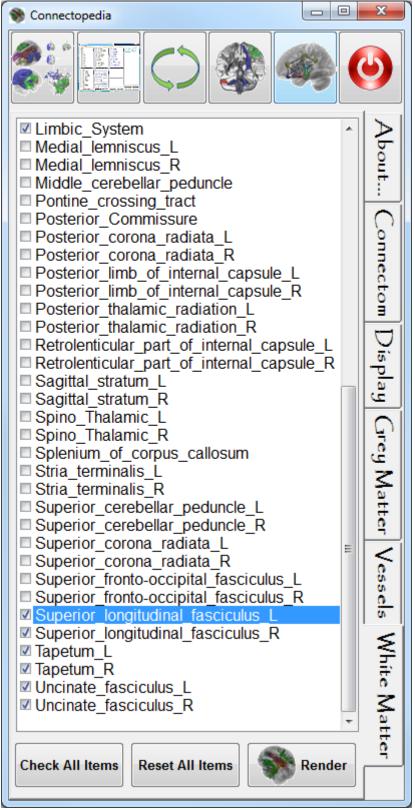
Connectopedia will detect the fiber bundles that are linking these two areas, here the "Cerebral\_Peduncle\_R" and the "Posterior\_Limb\_Internal\_Capsule\_R" by the cortico-pontocerebellar tract, and will display the found bundle(s) in the "Brain Ghost" sub-menu of the "Brain Views" Template 3D VR mode :



User can select from 2 to 116 cortical areas, but the more you select, the less you have chance to detect commun bundles (inclusive arithmetics).

# VIII. Fifth exercise: Virtual Dissection with "Anatomist" Drawings Rendering

Connectopedia includes a tool to perform virtual dissection in the "19<sup>th</sup> century anatomists" drawings fashion, either in color or black and white.



Let's start using the following White Matter Tracts, selected in the **White Matter Selector Tab** by LC on the empty square:

- Limbic System

- Superior Longitudinal Fasciculus R

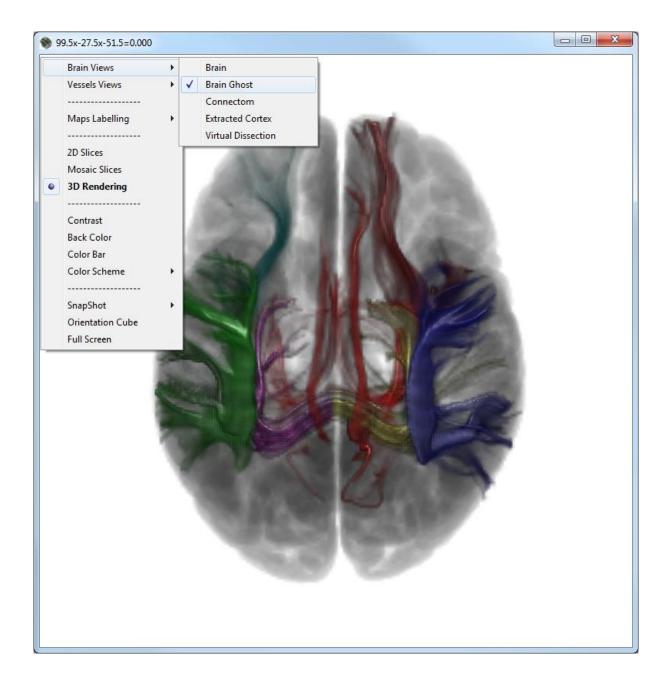
- Superior Longitudinal Fasciculus L

- Tapetum R

- Tapetum L
- Uncinate Fasciculus
- R

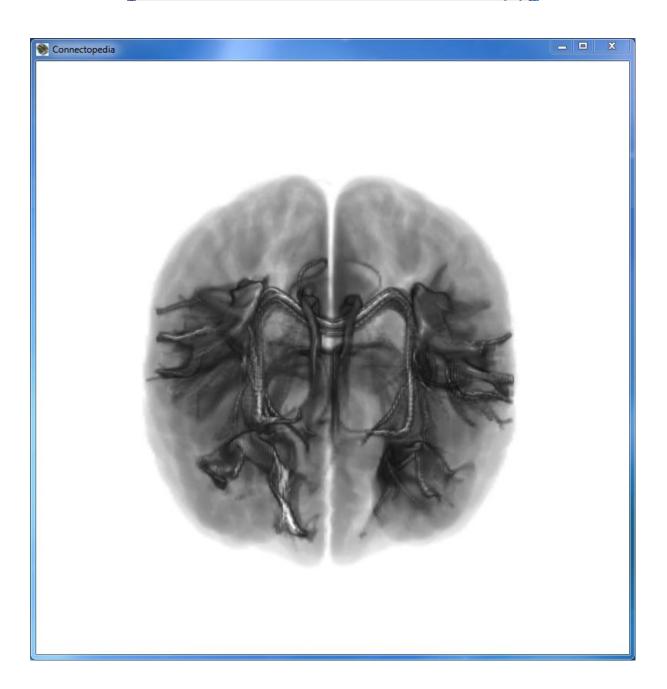
Uncinate Fasciculus L

Set the 3D Render window property to "Brain Ghost" sub-menu of the "Brain Views" menu Template, and press the Render button.

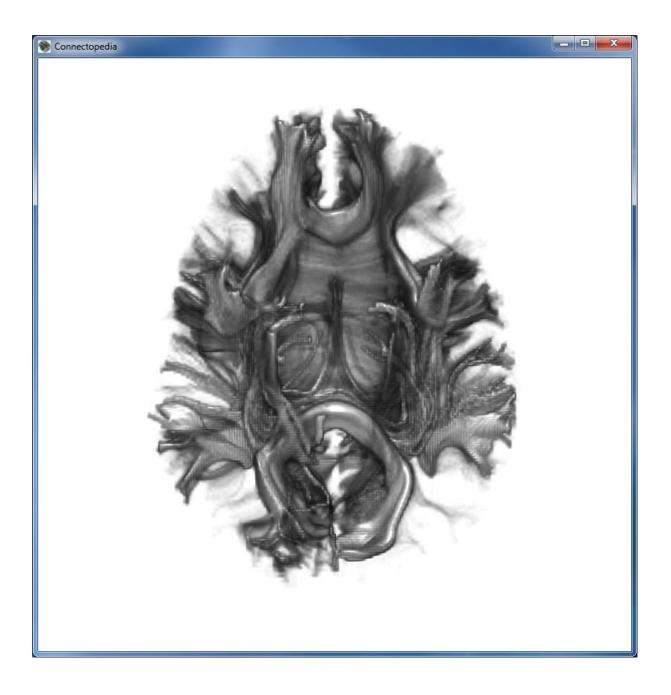


In the **Display Tab** of the **Selector**, set the "Alpha" property to 100 to render the selected bundles in Black and White.

Display	₽
Quality	out.
Alpha	<u>,</u>
Min Max	nnector
Uncinate_fasciculus_R    Red	Ξ

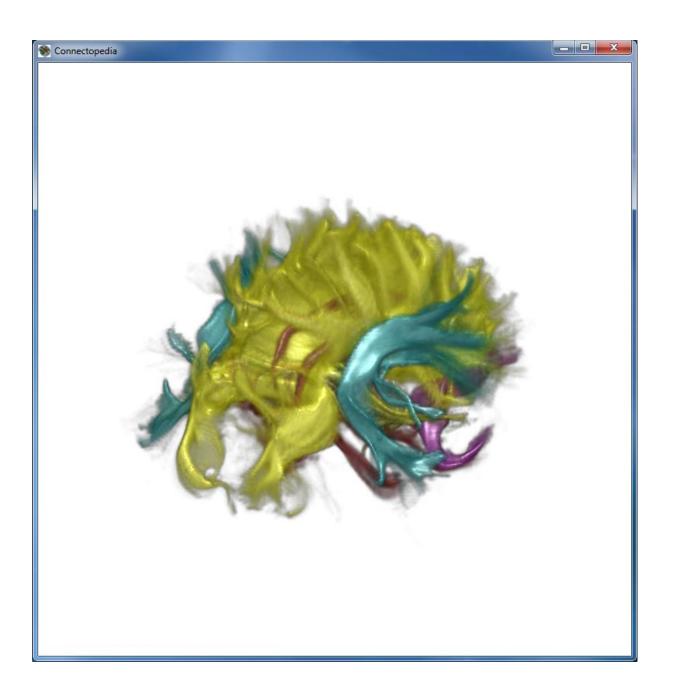


Then select the "Virtual Dissection" sub-menu of the "Brain Views" menu Template in the **3D Render** window to see the selected items without the outside brain. After the rendering, add the "Corpus Callosum" item by LC on the empty square in the **White Matter Tab** Selector, press the Render button, and set the "MinMax" property in the Display to to have a good quality rendering:



Set the "Alpha" property of the **Display Tab** to 50, and change the rendered color by selecting the reconstructed item and choosing the appropriate color:

Min Max	Min Max	onneo
Uncinate_fasciculus_R Violet [r+l  Corpus Callosum	Uncinate_fasciculus_R	→ iolet [r+b] →
Limbic_System (Superior_longitudinal_fasciculus_L Superior_longitudinal_fasciculus_R Tapetum_L		Grayscale Red Green تة Blue
Tapetun_L Tapetum_R Uncinate_fasciculus_L Uncinate_fasciculus_R	Clipping	Violet [r+b] Yellow [r+g]
Azimum	<u> </u>	Cyan [g+b]



## IX. Sixth exercise: Connectom Rendering

Connectopedia includes a tool to assess and render the brain functional and structural connectoms, based on its database entries.

Let's see which are the functional and structural connexions of the Limbic System.

Sonnectopedia		x
		9
<ul> <li>Parietal_Inf_L</li> <li>Parietal_Inf_R</li> <li>Parietal_Sup_L</li> <li>Parietal_Sup_R</li> <li>Postcentral_L</li> </ul>	*	About
<ul> <li>Postcentral_R</li> <li>Precentral_L</li> <li>Precentral_R</li> <li>Precuneus_L</li> <li>Precuneus_R</li> </ul>		Connecto
<ul> <li>Putamen_L</li> <li>Putamen_R</li> <li>Rectus_L</li> <li>Rectus_R</li> <li>Rolandic_Oper_L</li> </ul>		Connectom Display Grey Matter Ves
<ul> <li>Rolandic_Oper_R</li> <li>Supp_Motor_Area_L</li> <li>Supp_Motor_Area_R</li> <li>SupraMarginal_L</li> <li>SupraMarginal_R</li> </ul>		y Grey M
<ul> <li>Temporal_Inf_L</li> <li>Temporal_Inf_R</li> <li>Temporal_Mid_L</li> <li>Temporal_Mid_R</li> <li>Temporal_Pole_Mid_L</li> </ul>		latter Ve
<ul> <li>Temporal_Pole_Mid_R</li> <li>Temporal_Pole_Sup_L</li> <li>Temporal_Pole_Sup_R</li> <li>Temporal_Sup_L</li> <li>Temporal_Sup_R</li> </ul>	Е	sels
<ul> <li>☑ Thalamus_L</li> <li>☑ Thalamus_R</li> <li>☑ Vermis_1_2</li> <li>☑ Vermis_10</li> </ul>		White Matter
Check All Items Reset All Items	Render	<u>q</u>

In the **Grey Matter Selector** 

**Tab**, select by LC on theempty square:

- Amygdala R and L

- Cingulum Ant, Mid, and Post R and L

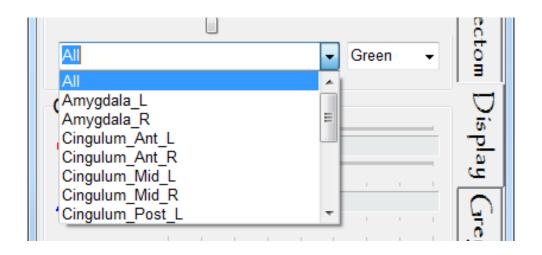
- Hippocampus R and

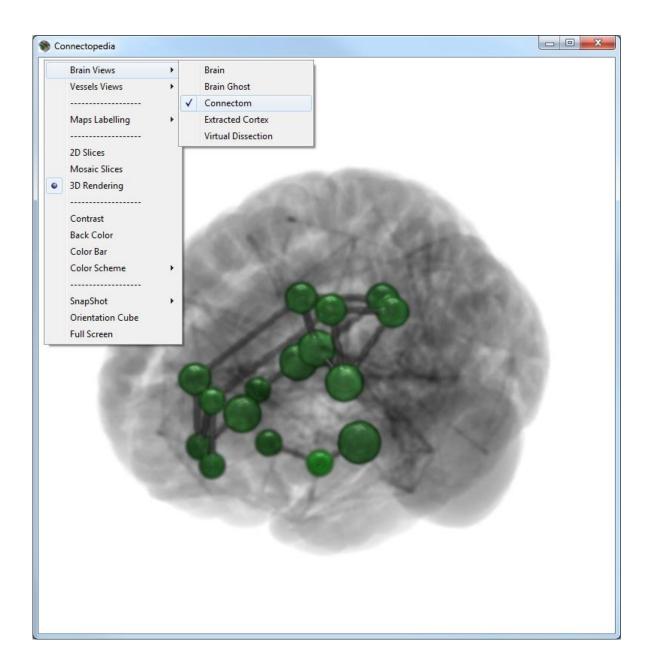
- L
  - Olfactory R and L
  - Rectus R and L
  - Thalamus R and L

Set the 3D Render window property to "Connectom" sub-menu of the "Brain Views" menu Template, and press the Render button.

In the "Display" Tab, select the Color Selector to "All" then "Green", to render the connectoms in green.

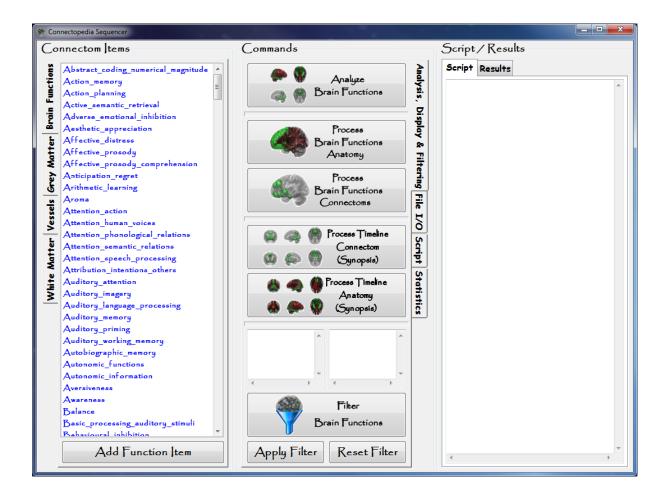
Whole brain structural connexions are shown in a skeleton line shape:





# XI. Seventh exercise: Script and Brain Functions Analyses

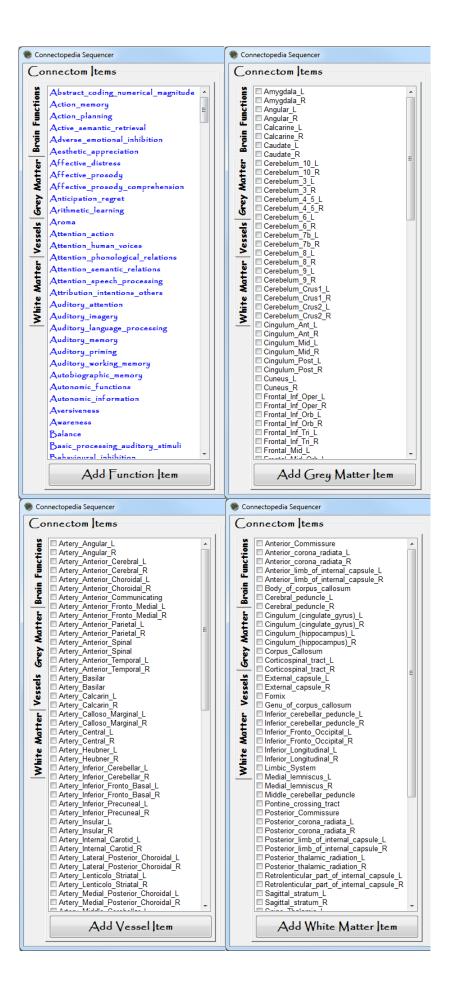
The **Connectopedia Sequencer** window lets users drive Connectopedia to script 3D reconstructions of the Brain Structures and to analyze Brain Functions.



There are Selector Tabs for Grey and White Matter, and Vessels structures, Brain Functions for filtering the analysis and Script Commands that can be batch processed or added to the "Script" window in the right part of the **Sequencer**.

By **RC** on the Buttons, users can choose between adding Structures to Script, or Functions to filter (inclusive "Add" or exclusive "Not").

Filters are applied or reset by **LC** on the appropriate Button, and Scripts can be Loaded, Saved, Cleared or Run also by **LC** on their respective Button in the '**Script**' Selector Tab.



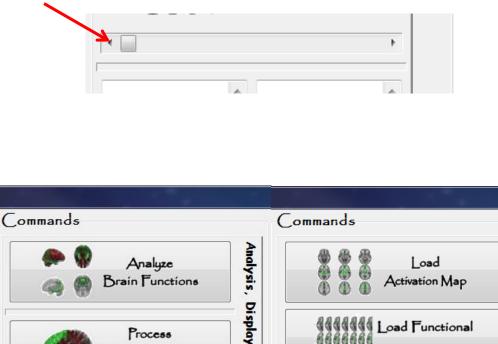
#### **XI.I Batch Commands**

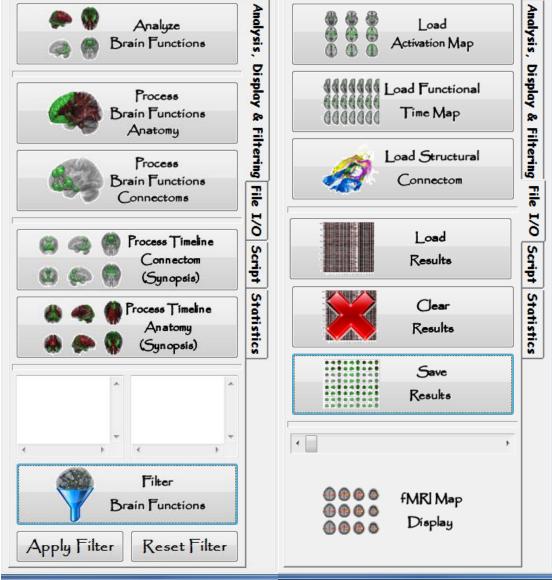
The 'Sequencer Window' has batch commands to Analyze Brain Functions, to Process Connectoms either of Brain Functions or from the Timeline fMRI acquisition, to Filter the Brain Functions using Grey and/or White Matter selected (checked) items, and Input/Output commands to Load or Save maps and results, and Scripts Commands further described.

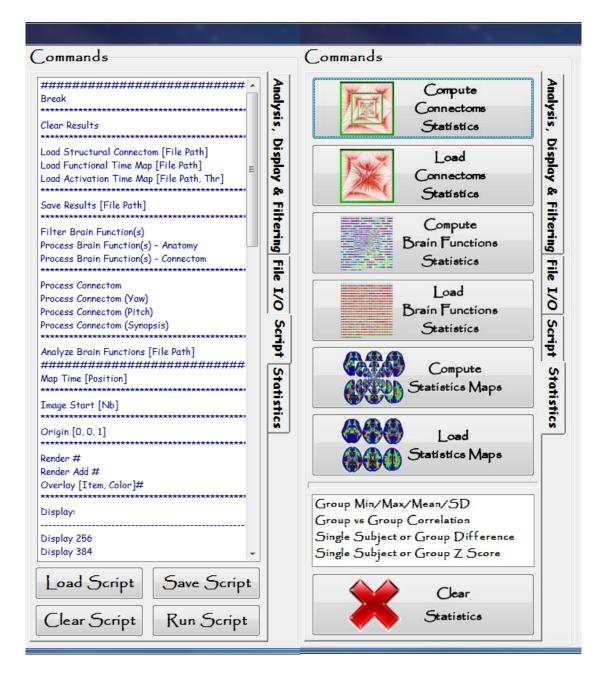
#### • Analysis, Display and Filtering Tab:

- 'Analyze Brain Functions' requires a Structural Connectom map file (.ctc) and a Functional Timeline Map file (.tta) created in DPTools (in the 'Connectomics' tab, by LC on 'Structural' or 'Functional' connectomic button).
- Process Brain Functions Anatomy', 'Process Brain Functions Connectoms' require a selected Brain Function in the 'Connectoms' Tab
- 'Process Timeline Connectoms (Synopsis)', 'Process Timeline Anatomy (Synopsis)', require a Functional Timeline Map file (.tta) created in DPTools
- 'Filter Brain Functions' will search for all Grey and/or White Matter Structures involved in different functions.
- File I/O Tab:
  - 'Load Results', 'Save Results', 'Clear Results' will load, save or clear the 'Results' Tab
  - 'fMRI Map Display' will display a previously loaded fMRI .ima file (-PST.ima) processed using DPTools
  - 'Load Activation Map' will load a fMRI .ima file (-PST.ima) processed using DPTools
- Script Tab:
  - Script to be executed, saved, clear or loaded.
- Statistics Functions :
  - 'Compute Connectoms Statistics', 'Compute Brain Functions Statistics',
     'Compute Statistics Maps' to compute Min/Max/Mean/SD, Correlation,
     ZScore, Difference of Single Subject or Group data.
  - 'Load Connectoms Statistics', 'Load Brain Functions Statistics', 'Load Statistics Maps' to load previously computed statistics.

In the 'File I/O & Filter' Tab, there are also Memoboxes for Boolean filter selections, and a scrollbar to scroll between the different timelines of a .tta file, showing all the Grey And White Matter items detected along the acquisition time.







### **XI.II Scripting**

Scripts commands are:

- *Break*: to stop the running script
- *Clear Results*: to clear the Results
- *Load Structural Connectom [File Path]*: to load the Structural Connectom, File Name and Path have to be provided
- *Load Functional Time Map [File Path]:* to load the Functional Connectom, File Name and Path have to be provided
- *Load Activation Time Map [File Path, Thr]:* to load the fMRI Activation Map in GIS format, either Global or in Real-Time ; File Name, Path and Threshold Value have to be provided
- Save Results [File Path]: to save to results of an analysis
- *Process Brain Function(s):* to generate a script for the Function Analysis dropped in the 'And Filter Box'
- Process Connectom: to generate a script for the Connectom Analysis
- *Process Connectom (Yaw):* to generate a script for the Connectom Analysis with Yaw rotations
- *Process Connectom (Pitch) ):* to generate a script for the Connectom Analysis with Pitch rotations
- *Process Connectom (Synopsis):* to generate a script for the Connectom Analysis with Synopsis Six views
- *Map Time [Position]:* to set the first Time Point of a fMRI activation map ; Integer value has to be provided (in number of TR)
- *Image Start [Nb]:* to set the number of the first image to be saved in the Movie Reconstructions ; Integer value has to be provided
- Origin [0, 0, 1]: to set the 3D rendering at the Origin view
- *Render #:* To Render the Grey, White Matter or Vessels structures ; Structures have to be added after the "Render #" and before the last "#" sign
- Render Add #: To Render the Grey, White Matter or Vessels structures in an "Additive" way ; Structures have to be added after the "Render #" and before the last "#" sign

- Overlay [Item, Color]#: to set the color of a rendered item ; Structures have to be added after "Overlay [Item, Color]#", followed by the selected Color ("Gray", "Red", "Blue", "Cyan", "Yellow", "Violet", "Green"), and before the last "#" sign
- *Display 256*: set the rendered display size to 256x256
- *Display 384*: set the rendered display size to 384x384 (default size for Synopsis Views)
- *Display 512*: set the rendered display size to 512x512
- *Display 720p*: set the rendered display size to 720p (1280x720)
- Arteries: to set the 3D rendering to the "Arteries" Template of the "Vessels Views" menu
- Brain: to set the 3D rendering to the "Brain" Template of the "Brain Views" menu
- *Brain Ghost*: to set the 3D rendering to the "Brain Ghost" Template of the "Brain Views" menu
- *Connectom*: to set the 3D rendering to the "Connectom" Template of the "Brain Views" menu
- *Cortex*: Brain: to set the 3D rendering to the "Extracted Cortex" Template of the "Brain Views" menu
- Veins: to set the 3D rendering to the "Veins" Template of the "Vessels Views" menu
- *Virtual Dissection*: to set the 3D rendering to the "Virtual Dissection" Template of the "Brain Views" menu
- Mosaic [Row, *Col, Orient, SlcNb]*: to set the 2D rendering Mosaic View of the selected Template ; Row number, Col number, Orientation (Axial, Coronal, Sagittal+, Sagittal-), Slice Labeling (0 or 1) values have to be provided
- MPR: to set the 2D rendering MPR view of the selected Template
- *Blue, Cyan, Gray, Green, Red, Violet, Yellow* colors for the Overlay [Item, Color]# script command
- *Rotation&Alpha #:* Command to set the Rotations (Yaw, Pitch, Yaw and Pitch, Synopsis) and Alpha variations of the 3D rendering reconstructions, with values:

-\*Yaw [Start, End, Nb Img]
\*Start: Starting value of the Yaw Rotation
\*End: Ending value of the Yaw Rotation

\*Nb Img: Number of images for one rotation

- \*Pitch [Start, End, Nb Img]

\*Start: Starting value of the Pitch Rotation
\*End: Starting value of the Pitch Rotation
\*Nb Img: Number of images for one rotation
-\*Distance [Nb Img]
\*Nb Img: Number of images for the distance variation
- \*Alpha [Start, End, Nb Img]
\*Start: Starting value the Alpha intensity
\*End: Ending value of the Alpha intensity
\*Nb Img: Number of images in between the intensity variation
#: Ending of the Rotation&Alpha # command
NB: if number of images rotations and number of images alpha variation are identical, the Alpha variation occurs during the rotation

- Snapshot: To take a single picture of the 3D Renderer Window
- *Alpha 3, Alpha 6, Alpha 12, Alpha 24*: Preset values for Alpha variation (3, 6, 12, 24 images)
- Yaw 90, Yaw 180, Yaw 270, Yaw 360: Preset values for Yaw rotations (90, 180, 270, 360 degrees)
- Pitch 90, Pitch 180, Pitch 270, Pitch 360: Preset values for the Pitch rotations (90, 180, 270, 360 degrees)
- *Yaw&Pitch 90, Yaw&Pitch 180, Yaw&Pitch 270, Yaw&Pitch 360*: Preset values for the Yaw and Pitch rotations (90, 180, 270, 360 degrees)
- *Single Bmp*: to save image into a single picture
- Synopsis Bmp: to save image to a six views Synopsis picture
- *Gif*: Video format for Animated GIF movies
- *MP4:* Video format for MP4 codec movies
- Create Movie [Path] : to create a movie ; File Name and Path have to be provided

#### Here is the script example for the Limbic System 3D reconstruction:

Origin [0, 0, 1]	#	RotationΑ #
Display 512	Overlay [Item, Color]#	*Yaw [Start, End, Nb Img]
Single Bmp	Olfactory_L	0
Brain Ghost	Green	360
Render #	Olfactory_R	30
Olfactory_L	Green	*Alpha [Start, End, Nb Img]
Olfactory_R	#	100

0 30 # Render Add # Rectus\_L Rectus\_R # Overlay [Item, Color]# Rectus\_L Green Rectus\_R Green # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Anterior\_Commissure Overlay [Item, Color]# Anterior\_Commissure Red # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Hippocampus\_L Hippocampus\_R Overlay [Item, Color]# Hippocampus\_L Green Hippocampus\_R Green # Rotation&Alpha #

\*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Amygdala\_L Amygdala\_R Overlay [Item, Color]# Amygdala\_L Green Amygdala\_R Green # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Limbic\_System # Overlay [Item, Color]# Limbic\_System Red # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Thalamus\_L Thalamus\_R # Overlay [Item, Color]#

Thalamus\_L Green Thalamus\_R Green # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Stria\_terminalis\_L Stria\_terminalis\_R Tapetum\_L Tapetum\_R # Overlay [Item, Color]# Stria\_terminalis\_L Red Stria\_terminalis\_R Red Tapetum\_L Red Tapetum\_R Red # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # ParaHippocampal\_L ParaHippocampal\_R # Overlay [Item, Color]# ParaHippocampal\_L Green ParaHippocampal\_R Green #

Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Uncinate\_fasciculus\_L Uncinate\_fasciculus\_R # Overlay [Item, Color]# Uncinate\_fasciculus\_L Red Uncinate\_fasciculus\_R Red # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Cingulum\_Ant\_L Cingulum\_Ant\_R # Overlay [Item, Color]# Cingulum\_Ant\_L Green Cingulum\_Ant\_R Green # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add #

Cingulum\_Mid\_L Cingulum\_Mid\_R # Overlay [Item, Color]# Cingulum\_Mid\_L Green Cingulum\_Mid\_R Green # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Cingulum\_Post\_L Cingulum\_Post\_R # Overlay [Item, Color]# Cingulum\_Post\_L Green Cingulum\_Post\_R Green # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Corpus\_Callosum # Overlay [Item, Color]# Corpus\_Callosum Red # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30

\*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Frontal\_Inf\_Oper\_L Frontal\_Inf\_Oper\_R # Overlay [Item, Color]# Frontal\_Inf\_Oper\_L Green Frontal\_Inf\_Oper\_R Green # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Superior\_longitudinal\_fasciculus\_L Superior\_longitudinal\_fasciculus\_R # Overlay [Item, Color]# Superior\_longitudinal\_fasciculus\_L Red Superior\_longitudinal\_fasciculus\_R Red # Rotation&Alpha # \*Yaw [Start, End, Nb Img] 0 360 30 \*Alpha [Start, End, Nb Img] 100 0 30 # Render Add # Heschl\_L Heschl\_R Angular\_L Angular\_R #

Overlay [Item, Color]# \*Alpha [Start, End, Nb Img] Heschl\_L 100 0 Green Heschl\_R 30 # Green MP4 Angular\_L Green Create Movie [Path] Angular\_R X:\Temp3\Limbic-Circuit-Yaw -----Green Gif # MP4 Rotation&Alpha # • \*Yaw [Start, End, Nb Img] -0 \*\*\*\*\*\* 360 \*\*\*\*\* 30 Analyze Brain Functions [File Path]

## **XI.III Brain Functions Analysis**

To analyze the Brain Functions of a specific task, user has to provide:

- The Structural Connectom map (.ctc file from DPTools processing)
- The Functional Timeline map (.tta file from DPTools processing)

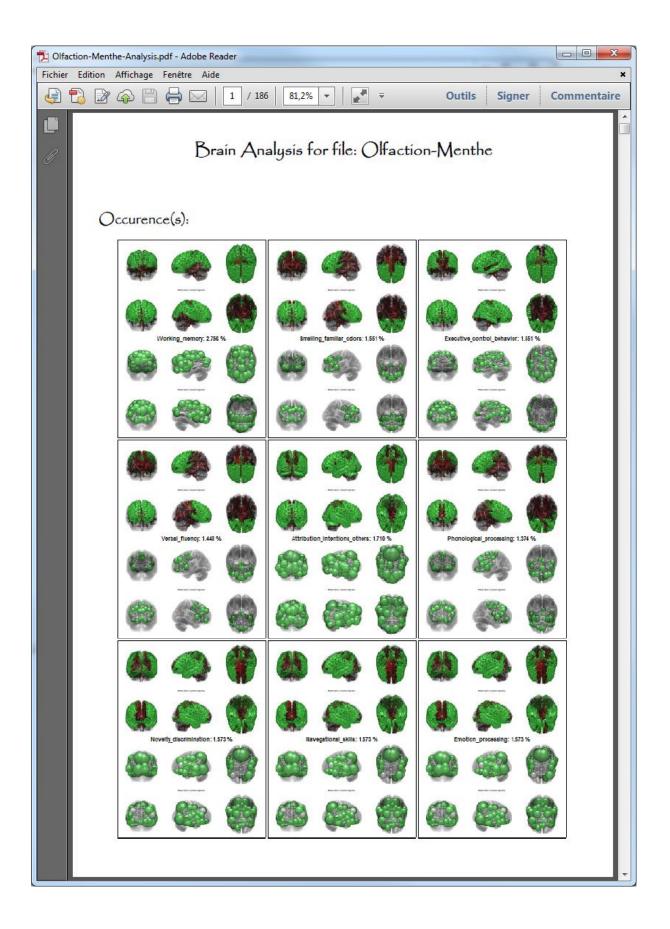
And either to set the script command: 'Analyze Brain Functions [File Path]' or 'Analyze & Render Brain Functions [File Path]' (far longer...) to the appropriate File Name and Path:

	x
Script / Results	
Load Structural Connectom [File Path] G:\Temp3\WMConnectom.ctc Load Functional Time Map [File Path] G:\Temp3\Menthe-TTA.ima Analyze Brain Functions [File Path] G:\Temp3\Menthe	*

Or by LC on the 'Analyze Brain Functions' / 'Analyze & Render Brain Functions' buttons in the 'Commands' 'Analysis & Processing' Tabs.

To focus on specific functions, user can add Functions to Filter by selecting them on the appropriate window, and LC on the "Add Function to Filter" Button. Then to press the "Run Script" Button.

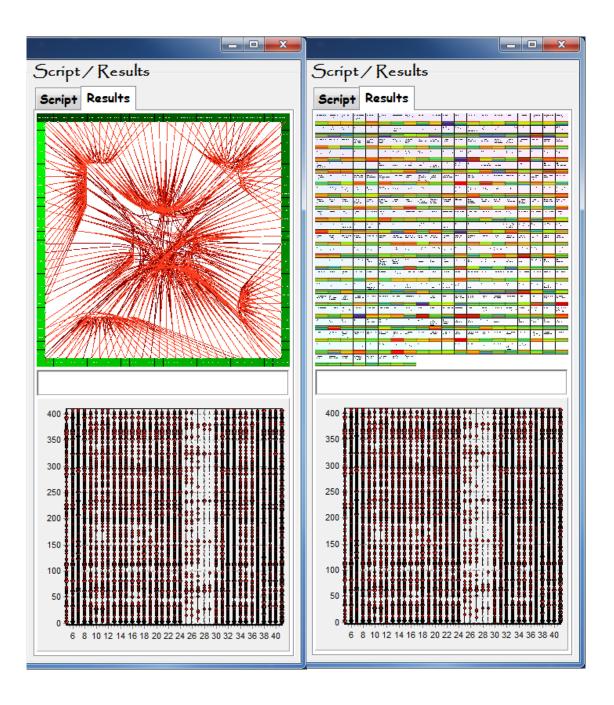
A pdf file will be generated with Major and Minor Brain Functions Occurences, and Timeline Brain Functions patterns:



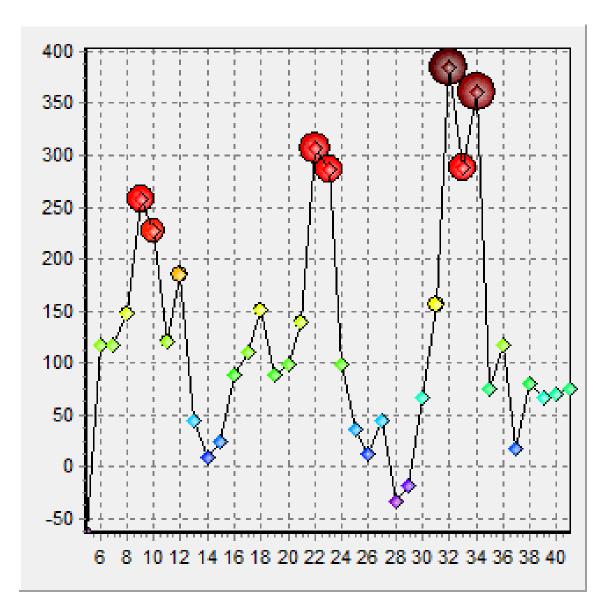
Dlfaction-Menthe-Analysis.pdf - Adobe Reader	_	
Fichier Edition Affichage Fenêtre Aide		×
🥥 🔁 🎧 💾 🖨 🖂 🛛 33 / 186 🛛 81,2% 🔹 🖌 👻 Outils	Signer	Commentaire
Brain Functions through Time:		^
**************************************		
Action_memory Anticipation_regret Attention_semantic_relations Attribution_intentions_others Auditory_memory		
Autobiographic_memory Aversiveness Awareness Breathing_control Categorization		
Color_structural_judgments_familiar_objects Courage Craving Decision_making Decision_making_involving_reward		
Deductive_reasoning Directional_information_head Drawing Dual_working_memory_task_processing Embarrassment		
Emotion_language_related Emotion_memory Emotion_processing Emotional_attachment Empathy		
Episodic_encoding Episodic_memory_retrieval Erotica Evaluative_judgment		
Experiencing_emotional_states Face_memory Face_name_association Face_recognition Fear_conditioning		
Finger_movements Forgiveability_judgment Happiness Humor_comprehension		
Hunger Identification_familiar_voices Inferential_reasoning Insight Integration_visual_elements_perceptual_wholes		

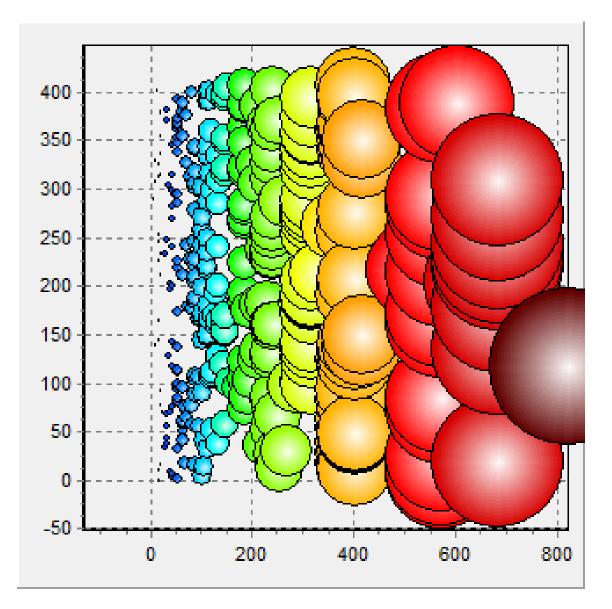
Other data are available in PDF or .xls files, and on graphs.

By Double Click on the Graph, user changes from Structural Connectomic View to Brain Function Usage:



When analysis is performed, by LC on either Grey Matter Item or Brain Function, Statistics of Function or Grey Matter Usage is displayed:





Attention komme voices	Basis processing anditory stimuli	Repid encod detection	Abstract coding numerical magnitude	Arathetic appreciation	Arithmetic Isoreing	Annai	Antibation intentions others	Anditory attention	Andreey prining	A	Balance	Debasisand inkikiting	Colcolotico	Cotogoriatine	Coollins monitoring	Desision asking	Desister making conflict reward	Desision making involving resard	Desizion antoriaisty
Minttheory	Mental time Leoping	Line biarction jedgenete	, Jaine attantion	leternal montal calculation	latention externel.	fataation farahask coaffict dataction	longht	leferential recenting	Jadantina ranaating	Goal intensive proceeding	Frequency design detection	Formation qualatation representations	Forginedailtay jadganat	Evaluation judgment	Eping	E erar detection	E	Daided attention	Deductive resources
Moral judgmente	Moral reasoning	Meltineking	Marie performane processing	Nonspatial anditory processing	Nerrerhal seconds presseding	Novelty discrimination	Orientation acleation attention	Perception Lowership to see	Perception proceed space	Perceptual priming	Precustions	Processing sharing patterns	Processing complex seconds	Processing discontinued accounting patterns	Processing rolated accortainty	Processing around intensity	Ressoring	Reasoning processes	Kecency judgenata
Affective proceedy	Alfective distress	Adverse emotional takihotan	Willedaction	Teathtsling	T capeal esterese	Stategy dauge response	Sound argragation	Soliing arithmetical tasks	Social parception	Seneory feadback conflict dataction	Selfreflection	Self referential throughts	Self other distinction	Sulf insight	Sons Alterat decrimination	Rick taking	Romand.	Response tons stimulus	Response inhibition
Allactive proceedy comprehension	Annainean	Courage	[	Emotion	Emotion processing	Emotion regulation	Emotional attachment	Emotional stimuli	Emotions and reflections decision making	Enganhy	Enpathy jadgment	Erotica	Especiancing emotional states	Faar conditioning	Тығ сыраны	Happianaa	Hernony	Hamor appreciation	Humar comprehension
Annatian phonological relations	* <b>,</b>	51	Response threat fearful atomica	Response anarativa attimati	Response antraine anditory atimalation	Roligious Fashing	Expension angelies canoticae	Processing emotions call reflections decision making	Processing constions decision making	Processing emotional stimuli	Pleasan	Plazant inplazant inotion	Panisk attack	Masia anjagunat	Mand oringe	Mond regulation	Madalating amotional response	Mirer estes egiten	<b>M</b> error <b>e</b> 1 area - 1
Attention connectio relations	Assessing agencies	Audinory larganga proceeding	Confirmations maning	Emotion Longuage related	Endertine emotional word	Expression sanctional information	Governating medicatic physics	Granneling contractor	Generation noloitee	lations.	Internally operation word generation	Leegenge comperimention production	freesening	Longoage weitching	Longoogo translation	Loughter	Louisel doctation	Lexisliafleation	Lucius annastis aubigaity processing
Semantic phorealogical Phoceog	Semantic monding	Sementic extegorization	Semantic ankigaity comprohension	Selective Attention speech	Kepone mintelligikle speech	Reception Longuage	Prosodie integration	Processing planalogical proportice words	Paraelagical ayatastis processing	Phonological processing	P	Perception presedie information	Orthography phraselegy lisk	Nonspeech processing	Neration comprehension	Mirror neurosa aparak parception	Metaphor comprehension	Literal seatean may relevation	Lexico ormantic processing
Semantic phonological processing	Sumartic processing	Seatence comprehension	Sentence attention	Speech attention	Speech competitionise	Spacek proception	Spoken language	Syntactic processing	Systectical processing	Yesh greation	Yorkal creationy	Yesbal cocoding non-remarkic process	Yorkal flacory	Yeekal threat detection	Word comprehension	Word generation	Attion memory	Active semantic retrieval	Auditory menny
Mamory convolution	M	Lasico comunic accaso maladas representatione	Lusical scarch	Learning tons based second largesge	Lursing	Lawa complex procedure	Irony processing	letertional forgetting	Mestification familiar voices	Event time based prospective memory	Epicodic memory retrieval	Epizodic long term memory	Epicodic according	Emotion memory	Daal working memory task processing	Declaration memory encoding	Correctore recollection	Astobiographic memory	Andresy working memory
Momory exceeding	Menning encoding recognition	Menory patters experition	Manary recognition	Monory estricual	Mermonic released	Maltinedal memory retrieval	Naming items learned early life	Negative atimali memory	New works! working memory	Processing matephone	Prospective memory	Reall digit series	Recognition	Rotainual unplaasant aaparisaana	Security memory retrieval	Seatence gameration	Shorttoon manory	Sabing covel probleme	Systectic working memory
Mirrar anarana grasping movemente	Mirror energia apreción moremente	Learning motor expresses	Kineathetin parception link moranaste	lekikisian blinking	Haricantal coccedic aga movemente	Exception control behavior	Discrimination finger gestares	Controlatoral Ioner link morenent	Controlotical lip torgan face month movement	Controlational Fingue band writet movement	Cheving	Binered manipulation	Westing memory	Ward retrieval opecific entities	Ward retrieval	Yechel nemory	(Ipdating verbal information	Tour felar memory recognition	Trapeod contest recognition
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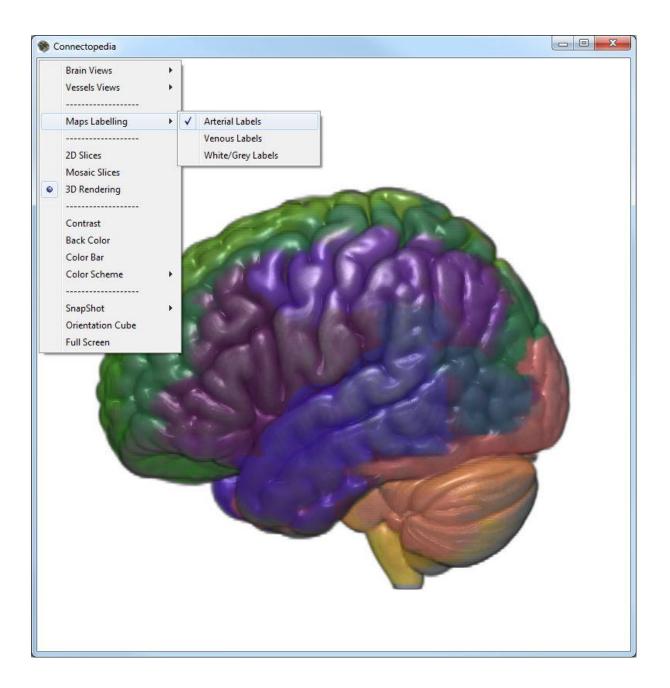
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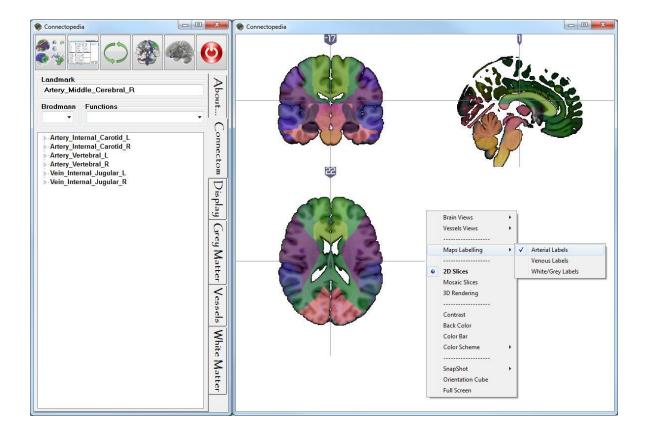
## XII. Eighth exercise: Labeling Anatomy, Arteries and Veins

The 3D Renderer window has a 'Map Labelling' menu with arterial, venous and grey/white matter structures maps which can be explored using the '2D Slices' menu.

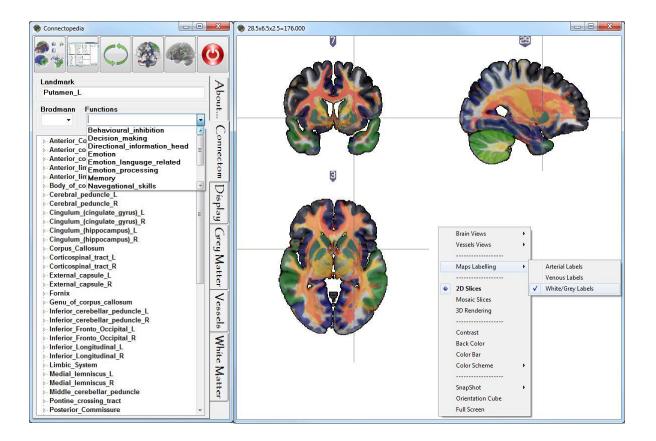
First, LC on the 'Arterial Labels' sub-menu of the 'Maps Labelling' menu item, then LC on '2D Slices' and display the 'Connectom Tab' in the 'Selector' window.

Then LC on a MPR reconstructed area in the 2D window ; the 'Landmark' label in the 'Connectom' tab will display the name of the pointed out structure.





When 'White/Grey Labels' is selected, the structure name is displayed as well as all the Brodmann areas and the Brain Functions where the pointed out structure is involved.



### XIII. Ninth exercise: Extracting Connectoms / Anatomy Pathways

The 2D Slices Menu using the 'White/Grey Labels' map template has a feature that enables the rendering of Anatomy or Connectoms pathways from a starting point Grey Matter area. By LC + hitting a special key on a grey matter area, all the structures that are connected to this area are displayed in an anatomic shape (key: 'CTRL') or in a connectomic shape (keys 'CTRL' + 'Left Shift' together).

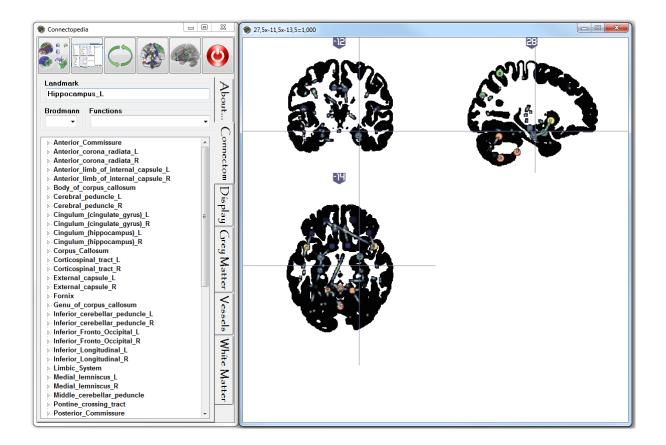
First select the 'Brain Ghost' template, then LC on '2D Slices' then 'White/Grey Labels', and LC on the Left Hippocampus (Label displayed in the 'Connectom' Tab:



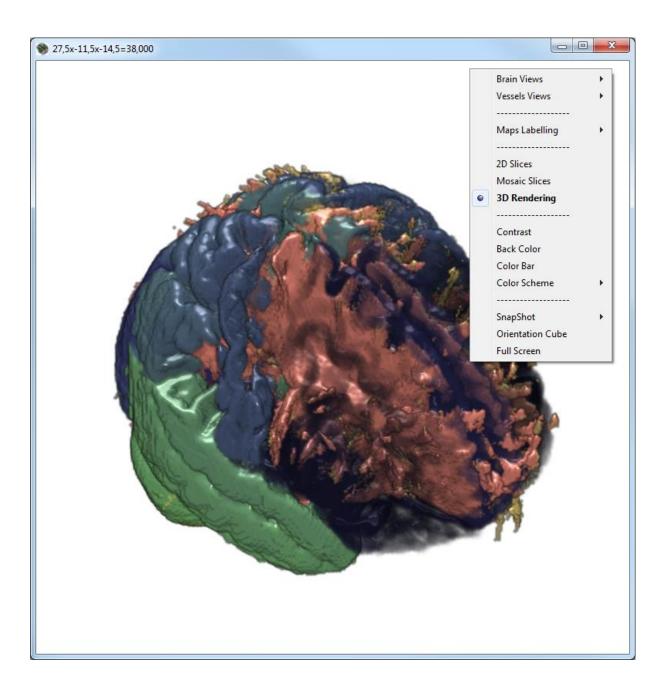
Then combine LC + 'CTRL' key on the same Grey Matter Structure to see the Anatomy Rendering of the connexions in 2D:



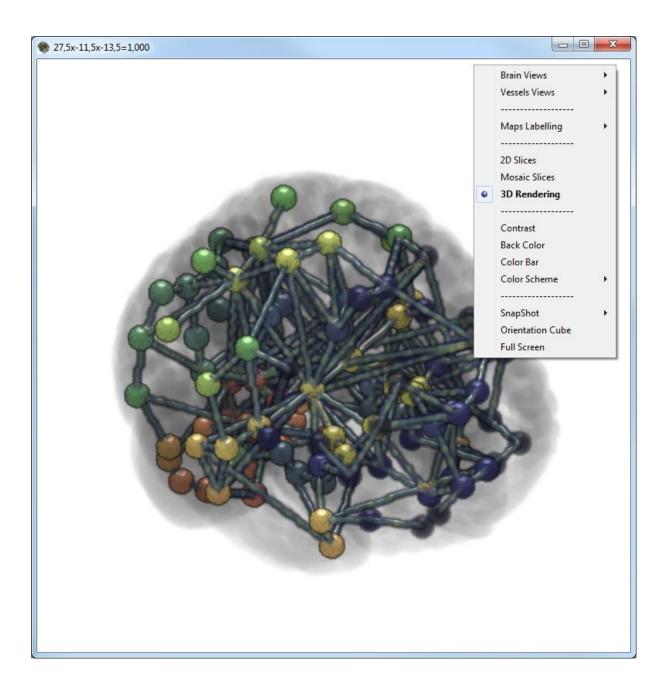
Or LC + 'CTRL' + 'Left Shift' to see the Connectoms rendering of the connections:



By LC on '3D Rendering' these reconstructions can be viewed in 3D mode, either for the Anatomy Rendering of the connections:



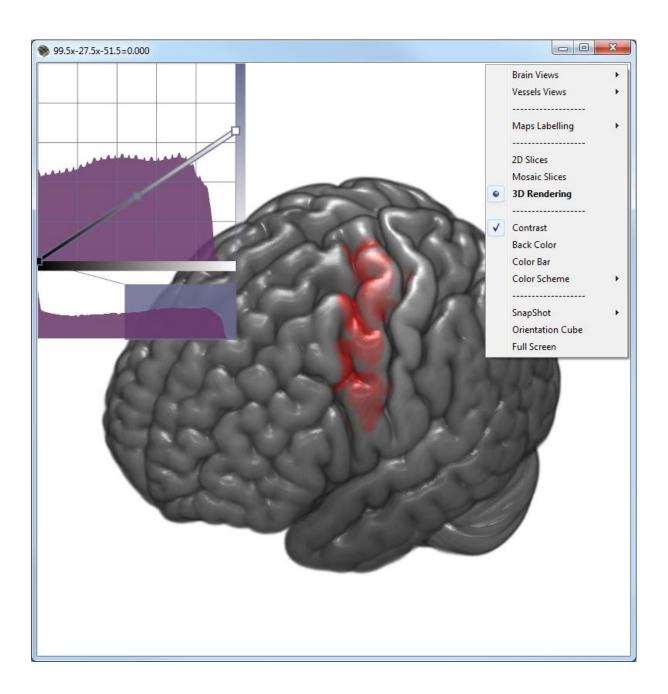
Or for the Connectoms Rendering of the connections :



# **XIV.** Other functions :

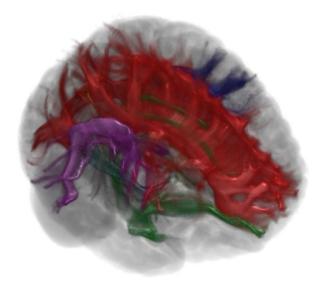
By LC on the 3D rendering area, user can:

- Set Contrast (by LC on it)
- Set Back Color (here white)
- Set Color Bar visible
- Orientation Cube visible
- Take a snapshot of the 3D Rendering area



User can view 3D Rendering area in « Full Screen »:

2.5x-17.5x-1.5=175.000



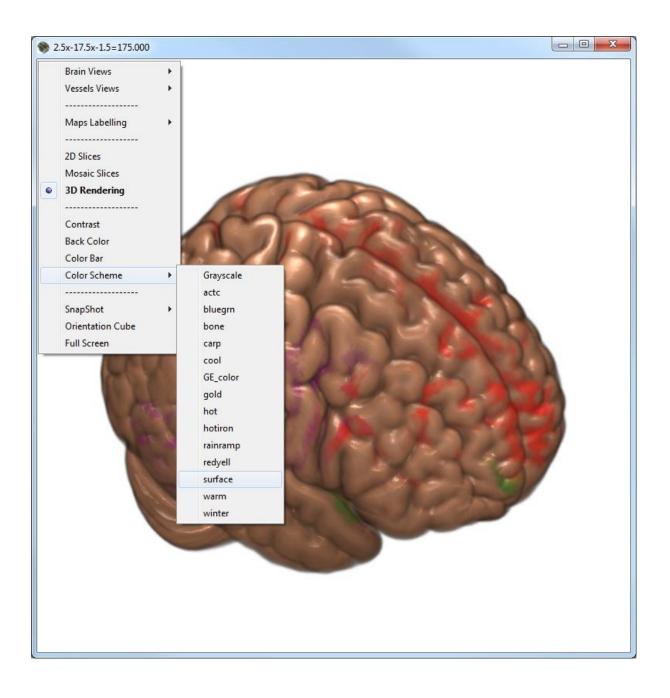


0 0 -X-

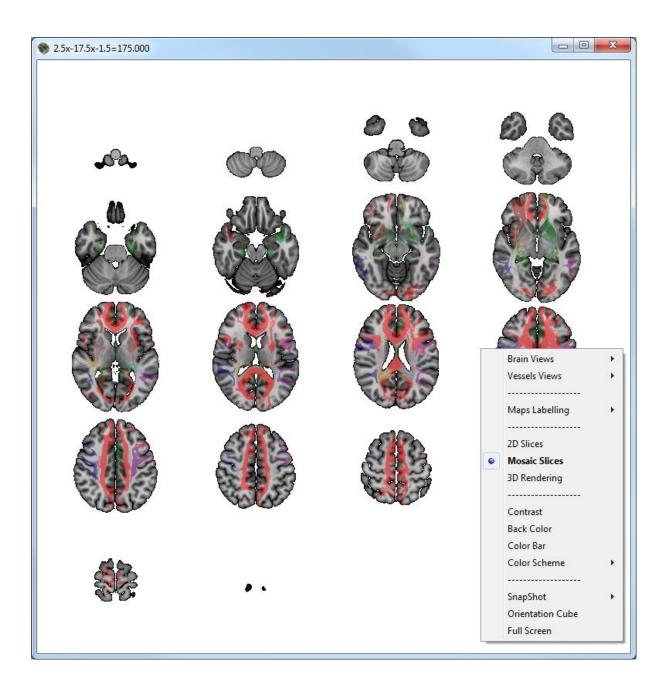


User can view in 2D MPR slices the selected items (WM, GM, and Vasculature):

User can set the 3D Rendering color reconstruction set by LC on « Color Scheme »:



User can view mosaic slices of the selected Bundles / Areas / Vessels by LC on « Mosaic Slices »:



Columns	4 🕤 5 🖨			
Rows				
Orientation				
Show cross slice			Label slice number	E
Script Command Copy Sc		Copy Script	Run Script	

User can select axial, sagittal, coronal reconstructions, and the number / pattern of the displayed slices.

### XV. Troubleshooting's

User might have some problems in installing or running Connectopedia. Here are some clues.

### **XV.I Connectopedia Windows Version:**

#### **xv.I.I Installation Shortcut**

After install, the link created in the "Start Program" menu of Windows might be erroneous.

Explore the files using "Windows Explorer" to see where Connectopedia have been installed (by defaut, "C:\DPTools\bin\Connectopedia"), then locate the "Connectopedia.exe" file. Create a symbolic link to the Desktop by Right-Click on it, then select "Send to…", then "Desktop (Create Shortcut)".

You should be able now to run Connectopedia by Double-Clicking on the link created on the Desktop.

#### **XV.I.II Running issues**

When Shortcut are erroneous, running Connectopedia can generate error messages at launch time, and Connectopedia can not be used.

Correcting the Connectopedia Shortcut (see section IX.I.I) generally solves this issue.

#### **XV.II Connectopedia OSX Version:**

Main issue with the OSX version is related to Mavericks GateKeeper, because Connectopedia is not signed as "Apple Approved" software yet.

Let's see how to overcome this issue (here "Onyx" software taken for example).

Starting with OS X Mountain Lion, Apple introduced a data execution prevention routine called Gatekeeper, which will block the automatic execution of programs that are either unsigned by an Apple Developer, or not issued through the App Store.

This routine prevents potentially malicious programs from running and harming the system or your data. However, while beneficial, it can also prevent legitimate programs from running, where it issues a warning that the program is not signed and will not allow it to run.



Warnings such as this will show when you attempt to open apps that are not signed, if you have Gatekeeper enabled on your Mac.

If you regularly use third-party programs that give this warning, then one option is to turn off Gatekeeper in the Security System Preferences, but this will prevent the service from helping secure your Mac.

To overcome this, there are two options. The first is to right-click the program and use the "Open" contextual menu item to initially launch such programs. The use of this menu suggests you explicitly intend to open the program, instead of perhaps inadvertently launching it with a double-click. When you do this, a warning message will still appear; however, if you choose the option to open the program, then a Gatekeeper exception will be made for it.



This message and button will appear in the Security & Privacy system preferences when you encounter an unsigned program.

If you have installed **OS X Mavericks** on your system, Apple has introduced another means for bypassing Gatekeeper. If you open a program that issues a Gatekeeper warning, then even if you have dismissed the warning, you can go to the Security pane of System Preferences, where you will see a message under the Gatekeeper settings about the recently blocked program. Next to this message is a button titled "Open Anyway," which if clicked, will launch the program and make an exception for it in the Gatekeeper database.

Even though the extra steps to use this new feature make it less convenient than using the contextual menu, it is still a new option for those using OS X Mavericks.

## XV.III OpenGl issues with Connectopedia Windows and OSX Version:

Both Windows and OSX versions of Connectopedia can be affected by a strange OpenGL issue due to the way OpenGl Shaders are rendered by the Video Card.

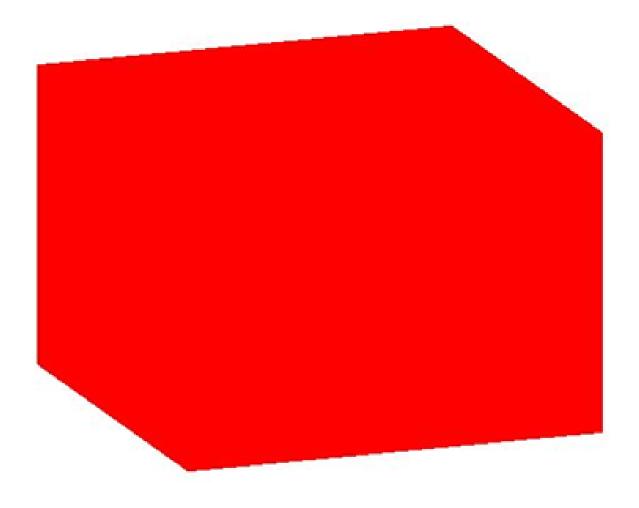
Brain can be rendered "deformed" such as:



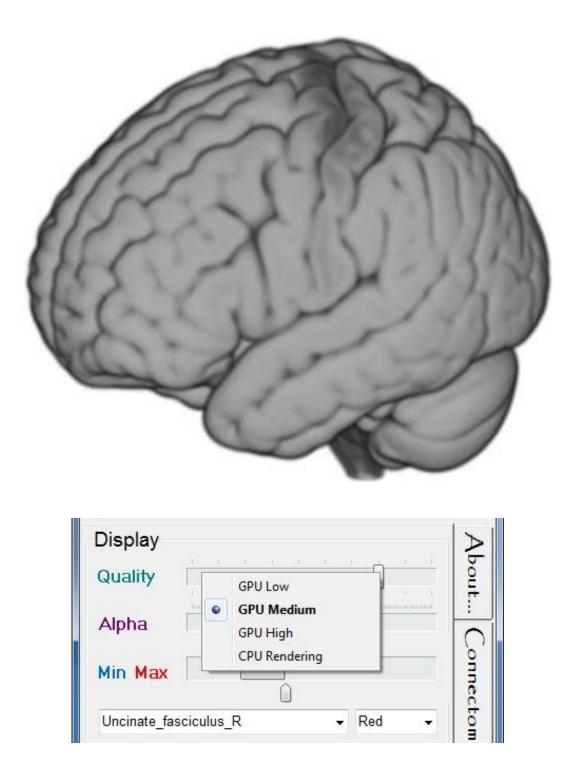
When user encounters this issue, closing then running Connectopedia again should correct this.



Other issues might also be encountered when the OpenGl drivers of the Video Card are incompletely implemented, e.g. when using VMWare Fusion on OSX for virtualization of the DPTools or Windows Standalone distribution of Connectopedia:



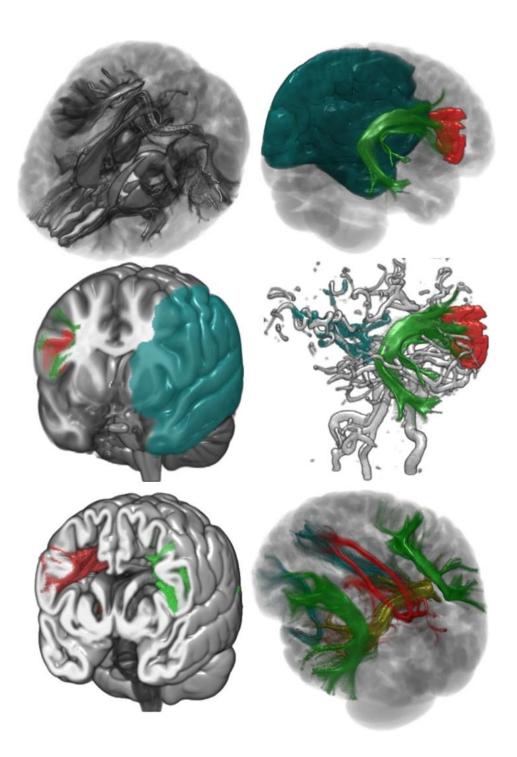
To overcome this issue, user can select different Rendering Quality, from "GPU Low" to "High Quality", and "CPU Rendering" by Right-Clicking on "Shader Quality" in the **Display Panel**.



All these issues are not exhaustive. If you have any pitfall or comment, please send an email to: denis.ducreux@fmritools.org

Visit <u>http://www.fmritools.org</u> to see Teaching Files and Videos related to Connectopedia.





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